

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:14:12 ; Search time 6073.61 Seconds  
(without alignments)  
4455.779 Million cell updates/sec

Title: US-08-656-055-18  
Perfect score: 5288  
Sequence: 1 GAATTCGCGGACGCCAAG.....TATGAAGAAAGCCCGAAT 5288

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 255875100 residues  
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: GenEmbl:  
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85: gb\_hc32:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	4681.6	88.5	6568	53	HSU43148
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 Bonifas, J. M., Quinn, A. G., Myers, R. M., Cox, D. R., Epstein, E. H. Jr. and  
 Scott, M. P.  
 Human homolog of patched, a candidate gene for the basal cell nevus  
 syndrome  
 Science 272 (5268), 1668-1671 (1996)  
 96247324  
 2 (bases 1 to 4344)  
 Johnson, R. L., Rothman, A. L., Xie, J., Goodrich, L. V., Bare, J. W.,  
 Bonifas, J. M., Quinn, A. G., Myers, R. M., Cox, D. R., Epstein, E. H. Jr. and  
 Scott, M. P.  
 Direct Submission  
 Submitted (29-MAY-1996) Departments of Developmental Biology and  
 Genetics, Howard Hughes Medical Institute Stanford University  
 School of Medicine, Beckman Center B300, Stanford, CA 94305-5427,  
 USA

## FEATURES

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Db	3301	GCTTTGGCCTTTCTGTACGGCCATCGCGCAGACAAACCCGAGGGCTGTGCTTGGCCCTGGAG	3360
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Db	3361	CACATGTTTGACACCCGCTCTCTGATGAGCGCCGCTGTCCACTCTGCTGAGATGCTGATGCTG	3420
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Db	3421	GGGGATCTGAGTTCGACTTTCATTTGTCAGGTATTTCTTTTCTGTGCTGGCGATCTCTACC	3480
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Qy	4044	TCCGATCTGGAGATATGATGTTCCGAGAGACAGTGTCAAGGGCTCCAGCGAGAGAGCTTCGGCAC	4103
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Db	3721	TACGAGGCCAGCAGAGAGGCGGGAGAGGCCCTGCCACCAAGTGTCTGTGAAGCCACAGAA	3780
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Db	4021	CCCTGGGGGGCCGCTTCTACCAACCCCTGTGGAGACCCAGCAGCTTCATGCTCATGTGGAGCTCC	4080
Qy	4464	GTGCGCGGCTACTGCGCAGCCCAATCACACTGTGACGGCTTCTGCTCCGCTGACTGTGGCC	4523
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Qy	4584	TACCTGTAGACTACCAACGCGCTGTGTTGAGAGACCCCAAGCTTTCACAGTCCGCTGT	4643
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 AUTHORS Scott, M.P., Goodrich, L.V. and Johnson, R.L.  
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 DB 717 ATACCTTTACCTTTGTTGATTAATACACCTTTGGACTCTTGTGGAAAGGGCGAAAGCT 776  
 QY 1106 ACAGCTGAGAGCAGATACCTCTGATGATTAACCTCTTGGGTGAGCAAACTTCGACCC 1165  
 DB 777 ACAGCTGAGAGCAGATACCTCTGATGATTAACCTCTTGGGTGAGCAAACTTCGACCC 836  
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 QY 1226 GCTGAATTAAGCTGAGGTGGTCAATGTTACATGGAACGCGCCCTGCTCAATCCGGCGA 1285  
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 QY 1406 GATTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1465  
 DB 1077 GATTGTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1136  
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OY	2306	CCCACCTCCCTACGACGCGACAGCTTTTCCCATGAAAGCGAGATTACCATGCAATGCCAC	2365
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OY	2366	TGTCCAGCTCCCGACGAGATATGACCCCCACACGACGCTATACACACCGCTAGACC	2425
Db	2037	CSTTACAGCTCCCGACAGAGATATGACCCCTTACACGACAGTGTACTACACACCGCCGAGCC	2096
OY	2426	GGCGTCCGAGATCTCTGTGCACGCCGTCAACCGTGAACACAGGACACCTCAGCTGCAGAG	2485
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OY	2486	CCCACGAGACACAGCTCCACAAAGGAGACCTGCTCCCAAGTTCTCCGACTCCAGCCCTCA	2545
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OY	2546	CTGCTCTGAGCCCCCTGTACGAGAGTGAGCACTCTCATCTTTTGTGTGAGAGCACTATAGC	2605
Db	2217	CTGCTCTGAGCCCCCTGTGACCAAGTGAGCACTCTCTGTGTTTGAAGAGCACTATAGC	2276
OY	2606	TCTTTTCTCTTTGAACCAAAAGCCAGGTAGTGGTGATCTTCTCTTTTGTGGGCTTGCT	2665
Db	2277	TCTTTTCTCTCTGAAACCCAAAGCCAGAGTTGGTGATCTCTTTTCTGTGGGCTTGCT	2336
OY	2666	GGGGGTCACGCTTTATGGGACCCACCGAGTGAAGAGAGGGCTGAGCTTACGGACATTTG	2725
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OY	2846	CTTACACAGAGAGTTTCAAGTACGTAAGTGTATGATTTGGAAGAAACAAACAGCTTCC	2905
Db	2517	CCTTCTTAAGAGAGTTTACGCAATGTGAAGTATGTATCTGTGAGSAGAACAAAGCACTTCC	2576
OY	2906	CAAAATGTGGCTGCACTACTTTCAGAGACTGGCTTCAGGAGCTTCAGAGTGCATTTGACAG	2965
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OY	2966	TGACTGTGGAGAACCGGGAATACTATGCCAAACATTTACAAATATGATCAAGACATGGAGT	3025
Db	2637	TGACTGTGGAGAACCGGAGAGTCACTATGCCAAACATTTAAATAATGATCAAGTCAAGGGGT	2696
OY	3026	CTTGCTCTCAAACTCTCTGGTGTGAAACCGGACGCGGATTAAGCCCATTCGACATCAACCA	3085
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QY	3866	CCTGGCGCTTCTCAATGGCTGTGCTTTCCTTCCGCTTTTGTCTTTCTTTGGACATA	3925
Dp	3537	CTTGGGGGTTCTCAATGGATGCTTTCGCTGCGCTGTCTCTTATCTTTTGGACCGTG	3596
QY	3926	TCTTGAGGTGTCCAGGCCAAGGGCTTGAACCGGCTGCCACACCCCTCCCTGGAGCAC	3985
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QY	3986	CCCGACGATGTCGCTTGCCATATGCCGCCCGGCGCACAGCGGGGTCTGATTTCTC	4045
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QY	4046	CGAATCGGAGTATAGTTTCCAGACAGACAGTGTACAGGCTTACGAGAGAGCTTGGGACTA	4105
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VERSION AR055791.1 GI:5981368
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5187)
AUTHORS Scott, M.P., Goodrich, L.V., and Johnson, R.L.
JOURNAL Patched genes and their use
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Db	2157	TCCCGAGAGAGCACAGCTCTACAGAGGACCTGCTCCAGTTCTCAGACTCCAGCTCAG	2218
Qy	2546	CTGCGTGTAGAGCCCCCTGTGTACGAAGTGACACTCTATCTTTGCTGAGAAACACTATGC	2605
Db	2217	CTGCGTGTAGAGCCCCCTGTGACCAAGTGACACTCTCTCTGTTGAGAGAACTATATGC	2276
Qy	2606	TCCCTTTCCTGTGAACCAAAAGCCAGAGTGTGTGTATCTCTCTTTTCTGTGGCTGTCT	2665
Db	2277	TCTCTTCTCTCTGAAACCCCAAGCCAGAGTTGTGTATCTCTTTCTGTGGCTGTCT	2336
Qy	2666	GGGGGTACGCTTTATGTGGCACACCCGAGTAGAGAGAGGCGCTGTGACCTTACGACATGT	2722
Db	2337	GGGGGTACGCTTTATGTGGACACCCGAGTAGAGAGAGGCGCTGTGACCTCAGGACATGT	2390
Qy	2726	ACCTCGGGGAAACCGAGAAATATGACTTTATGTGTGACAAATTCAAATTCCTTCTCTTA	2785
Db	2397	TCCCGGGGAAACCGAGAAATATGACTTTATGTGTGACAAATTCAAATTCCTTCTCTTA	2456
Qy	2786	CAACATGTATATATAGTACACCGAGAACGAGATACCCCAATATCCAGCACTTACTTTAGCA	2845
Db	2457	CAACATGTATATATAGTACACCGAGAAAGAGATATACCCCAATATCCAGCACTTACTTTAGCA	2516
Qy	2846	CTTACACAGAGATTTTCACTGTAAGTGAAGTATGTATGTTGGAGAGAAACAAACAGCTTCC	2905
Db	2517	CTTTCATTAAGAGTTTCAGCAATGTGAAGTATGTATGCTGTGAGAGAAACAAACAGCTTCC	2576
Qy	2906	CAAAATGTGCTCCTACTACTTCAAGAGAGCTGCTCAGAGAACTTGAAGTGTGATTTGACAG	2965
Db	2577	CGAAATGTGCTCCTACTACTTCAAGAGAGCTTCAAGTGTGATTTGATTTGACAG	2636
Qy	2966	TGACTGGGAAACCGGGGAAATCATGCCAAACATTTACAGAGATGATCAGACATGAGAGT	3025
Db	2637	TGACTGGGAAACCTGGAGATCATGCCAAACATTTAAATAATGTGATCAGATGACGGGGT	2696
Qy	3026	CCCTGGCTACAAATCCTCGTGGGAAACCGCGACCGCGGATATAGGCCATTCGACATCAGCA	3085
Db	2697	CCCTGGCTACAAATCCTCGTGGGAAACCGCGACCGCGGATATAGGCCATTCGACATTAATCA	2756
Qy	3086	GTTTACTAAACAGCGTCTGTGTGATGACAGATGAGTATTAATTCAGAGCTTTCATCAT	3145
Db	2757	GTTTACTAAACAGCGTCTGTGTAGACGAGATGAGTATTAATTCAGAGCGCTTTCATCAT	2816
Qy	3146	CTTACCTGAGAGGCTTGGGTCAAGCAACGACCCCGTGGCTATGTCTCCATCCAGGCCAAT	3205
Db	2817	CTTACCTGAGAGGCTTGGGTCAAGCAACGACCTGTATGCTTACGTCTCCAGGCCAAT	2876
Qy	3206	CCGGCCACACCGACCAAGATAGGGTCCACGACAAAGCCGACATCATGCGCTGAACCAAGCT	3265
Db	2877	CCGGCCACACCGCGCGAGTGGGTCCATGACAAAGCCGACATACATGCCAGAGACCAAGCT	2936
Qy	3266	GAGATATCCGGCAGCAGAGCCCATCGAGTATGCCAGTTCCCTTCTTACTCTCAACGGGT	3325
Db	2937	GAGATATCCGACAGCAGAGCCCATCGAGTATGCCCTGAGTTCCCTTCTTACTCTCAACGGCT	2996
Qy	3326	GGGGGACACTTCGACTTTTGTGAGGCAATTTGAAAAAGTAAAGACATTCGACAGCACTA	3385
Db	2997	AGGAGACACTCAGACTTTTGTGAAAGCATAGAAAAAGTAAAGTATCTGTAAACATTA	3056
Qy	3386	TAAGAGCTTGGGGCTGTCCAGTTTACCCCAAGGCTACCCCTTCTCTTCTGTGGAGAGCTA	3445
Db	3057	TAAGAGCTTGGGGCTTCTCCAGCTTACCCCAATGAGCTACCCCTTCTGTGTGGAGGCAATA	3116

QY	3446	CATCGGCGCTCCGCCACTGGCTGCTGCTGTTCAATACAGCGTGTGGCCCTGCACATTCCT	3505
QY	3446	CATCGGCGCTCCGCCACTGGCTGCTGCTGTTCAATACAGCGTGTGGCCCTGCACATTCCT	3505
Db	3117	CATCAGCCCTGGCCCACTGGCTGCTGCTATCCATCACAGCGTGGTGGCTGCACGTTTCT	3176
QY	3506	CGTGGCCCTGTCTTCTCTTCTTACACCCCTCGAGAGGCGGGGATCATGTGATGGTCTGGC	3565
Db	3177	AGTGGCGCAGTCTTCTCTCTGACCCCTCGAGAGGCGGGGATCATGTGATGGTCTGGC	3236
QY	3566	GCTGATGACGCTCGAGCTGTGGGCATGATGGGCCATTCGGAATCAAGCTCAAGTGGCCT	3625
Db	3237	TCTGATGACCGCTGGAGCTCTTGGCATGTGATGGCCATTTGGGATCAAGCTCAAGTGTGT	3296
QY	3626	GCCCGTGGATCCAGTCGATGCTGCTTGTGGCATAGAGAGTGAAGTCAACCTTACGTTGC	3685
Db	3297	GCGTGTGGATCCAGTCGATGCTGCTTGTGGCATAGAGAGTGAAGTCAACCTTACGTTGC	3356
QY	3686	TTTGGCCTTTCGACGGCCATGCGGCACAAGAACCGCAGGCGTGTGTTGCCCTTGAGACA	3745
Db	3357	TTTGGCCTTTCGACAGCCATTGGGGACAAAGAACCAAGGGCTATGCTCCTCTGGAAACA	3416
QY	3746	CATGTTTGGACCCGTCCTGGATGGCGCCCGTGCACATCTGCTGGAGATGCTGATGCTGGC	3805
Db	3417	CATGTTTGTCTCCGTTCTGGACGGTGTGTGTCTACTGTCTGTGGTGTACTGATGCTTGC	3476
QY	3806	GGGATCTGAGTTGACTTCATTGTCAAGTATTTCTTGTCTGTGCTGGCGATTCCTACCAT	3865
Db	3477	AGGGTCCGAAATTTGATTTATTCATTCAGATACATCTTGTGGCTGCTGGCCATTCCTACCGT	3536
QY	3866	CGTGGCGCTTCACANTGGGCTGGTTTGGTTCGCCGAGCTTTCGCTTCTTTGGACCATTA	3925
Db	3537	CTTGGGGGTTCTCANTGAGCTGTTGTCTGTGCTGCTGTCTTATCTTCTTTTGGACCGTG	3596
QY	3926	TCCTGAGCTGTCTCAGCCAAAGCGGCTTGAACCGGCTGGCCACACCTCCCTCGAGCCACC	3985
Db	3597	TCCTGAGGCTGTCTCCAGCCAAATGGCTCTAAACCCAGTGCACATCTTCCGCTTGAGCGCGC	3656
QY	3986	CCCCAGCGGTGCCGTTGGCCATGCGCGCCCGGCCACAGCCACAAGGGGGTCTGATTCCTC	4045
Db	3657	TCCAACTGTGTCGCGGTTTGGCTGCTGCTCTCTGTGTCAACCAACATGGGTGTGATTCCTC	3716
QY	4046	CGACTCGAGATATATGTTCCACAGACAGACAGTGTAGAGGCTTCAGGAGGAGGTTCCGACATA	4105
Db	3717	CGACTCGAGATACAGTCTTCAGACACAGGGTGTGGCATAGTGGAGGCTCAGGACATATA	3776
QY	4106	CGAGGCCCAAGCAGGCGCGCGGAGGCCCTGCCCAACCAAGTATCTGTGAAGCCACAGAAAA	4165
Db	3777	CGAAGCACACGACAGGTCGCGGAGGCCCCGCCACCAAGTATGTGTGAAGCCACAGAAAA	3836
QY	4166	CCCGCTCTTTCGCCACTCTGCATCTGTGTCTATCCCGAATCCAGGCAATACCACCCCTCGAA	4225
Db	3837	CCCGTCTTTCGCCCGGTCACCTGTGGTCATCCGGAGATCCAGACATCAGCCTCCCTTGAC	3896
QY	4226	CCCGAGACACAGCCCCCACTGGACTCAGGCTGCTCTCCCGGACAGGACAGGCCACGA	4285
Db	3897	CCCTCGGCAACACCCCACTGAGCTCTGCTCTCTTCCCTGGAGCGGACAAGGCCACGA	3956
QY	4286	GGCCCCGACAGGACCCCCCGAGAAAGGCTGTGGCCACCCCTACACAGCCGCCACAGA	4345
Db	3957	GCGTCCAAAGGATCCCCCTTAGAAGAGGCTTGGCGCACCCCTTACAGACCGGCCACAGA	4016
QY	4346	CGCTTTGAAATTTCTACTGAAGGCAATTTGGCCCTAGCAATAGGGCCGCGCTGGGGCCC	4405
Db	4017	CGCTTTTGAATTTCTACTGAAGGCAATTTGGCCCTAGCAATAGGGCCGCGCTCAGGGCC	4076
QY	4406	TGCGGGGGCGCGTTTCTACAAACCTCGGAACCCAGGCTCACTGCCATGGGCACTCGCT	4465
Db	4077	CGGTGGGGCGCGTTTCTACAAACCTCGGAACCCAGGCTCAACGCCCATGGGCACTCTGT	4136
QY	4466	GGCGGGCTACTGGCAGGCCCTACACACTGTGAGCGGCTTTCGCTCCGAGCTATGTCGGCCT	4525
Db	4137	GGCCAGCTACTGGCAGGCCCATCACCACTGTGACGGCTTCTGCTTCGGTGTGACTGTGGCTGT	4196

QY	4526	GCACCCGGCCGCTGTCCTGGGCGTGGGGGAGAACCCCCAGAGGGGGACTCTGGCCAC	4581
Db	4197	GCATCCCCCG-----CTGCACTGGGCGCAACCCCCGAGGGGGCCCTGTCACAGGCTA	4250
QY	4582	-----GCTACCCCTGAGACTGACCAAGGCCCTGTTTGAGAGCACCCCACAGTCCCTTCACAGT	4636
Db	4251	TCGAGAGTACCTCGAGACTGATCAACGGGGGTATTTTGAGGATTCCTCATGTGCTTTTCATGT	4310
QY	4637	CCGGTGTGAGAGAGAGGATTCGAAAGTGAACATCATGTGAGTGGCGAGAGCTGGAAATGGCA	4696
Db	4311	CAGGTGTGAGAGAGAGGACTCAAGGTGGAGGTCATGAGACTACAGAGAGCTGGAAATGTGA	4370
QY	4697	GGAGAGGCCCGGGGGAAGCAGCTCCAACTCAGAGGTGATTTAAATCATCTGAAGCAAAAGAGCC	4756
Db	4371	GGAGAGGCCCGTGGGGAGAGCACTCCAACTCAGAGGTAAATTTAAATCTGAAGCAAAAGAGCC	4430
QY	4757	AAAGATTTGAAACCCCCACCCCCACACTCTTTTCAGAACTGCTTGAAGAAAGAACTGGTTGG	4816
Db	4431	AAAGATTTGAAA--GCCCGCCCCCACCTTTTCCAAACATGCTTGAAGAAAGAACTGCTTGG	4489
QY	4817	AGTTATGGAAGAAAGATGCCCCCTGTGCCAGCAGCAGTTCATTTGTTACTGTAAACGATTTGA	4876
Db	4490	AATTTATG-----GGAAAGGAGTTCAATGTTACTGTAAACGATTTGA	4530
QY	4877	TTATTTTGTAAATATTTCTATATAATATTTTAAAGATGTACACATGTGTAAATATAGAAAG	4936
Db	4531	TTATTTTGTGAAATATTTCTATATAATATTTTAAAGGTGTACACA--TGTAAATATACATGG	4588
QY	4937	GAAAGATTTAAAGTGTATGATCTGGGGCTTCCCACTCCTCGCCAGAGTGTGAGAGCC	4996
Db	4589	AAATGCTGTACAGT--CTATTTCCTGGGGCTCTCCACATCTCTGCCAGAGTGGGAGAGCC	4647
QY	4997	ACAGTGGGGCTCTCCGTAATTTGTGCAATTTGGCTCCGTGCCACACCAACGCTTCATTAGT	5056
Db	4648	ACA--GGGGCCCTTTCCCTGTGTACATTTGCTCTGTGTGCCAACCAACGCTTCATTAGT	4705
QY	5057	CTTAAA-----TTTCAGCATATGTGGTGGTGTAAATTTGTATATTTACTTGT	5108
Db	4706	TTTTTAAAAAATCTCCACGATATGTGGTGGTGTAAATTTGTATATTTACTTGT	4765
QY	5109	ATAATTTCTATGCAAAATATTTGCTTATGTATATAGCATTTATTTTGTAAAGTTCCTGTTTAA	5168
Db	4766	ATAATTTCTATGCAAAATATTTGCTTATGTATATAGCATTTA--TTTGTAAAGTTCCTGTTTAA	4824
QY	5169	ATAATTTTAAATTTGCATATCACAGCCCTGGTGAATGAGTAAATGTTACTGTTAACTTTCA	5228
Db	4825	ATAATTTTAAATTTGCATATCACAGCCCTGGTGAATGAGTAAATGTTACTGTTAACTTTTG	4884
QY	5229	AACACGCTATGCGTGTAAATTTTGTGTTTAAATGAGCAGATATGAGAAAGC	5280
Db	4885	AACACGCTATGCGTGTAA-----TTGTTAAGAGAGACATGAGAAAGAAC	4931
RESULT	6		
LOCUS	MMU046155	4305 bp	31-DEC-1998
DEFINITION	MMU046155	Mus musculus patched mRNA, complete cds.	
ACCESSION	U46155		
VERSION	U46155.1	GI:1181884	
KEYWORDS			
SOURCE		house mouse.	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS		Goodrich,L.V., Johnson,R.L., Milenkovic,L., McMahon,J.A. and Scott,M.P.	
TITLE		Conservation of the hedgehog/patched signaling pathway from flies to mice: induction of a mouse patched gene by Hedgehog	
JOURNAL		Genes Dev. 10 (3), 301-312 (1996)	
MEDLINE		96176226	
REFERENCE		2 (bases 1 to 4305)	
AUTHORS		Scott,M.P.	



Db	1041	AAACATGTTCCAGTTAAATGACATCCCAAGCAAAATGATGAACACTPCAGGGGGCTACACACTA	1100
Qy	1526	TGTCCTCACACATCAACCTGAGACGAGACAAAGCGGACGCCATCTCTGGAGCCCTGGCAGAG	1585
Db	1101	TGTCCTCTCAATCAACCTGGAATGAAGACAGGGGAGCGGCCCATCTCTGGAGCCCTGGGAGAG	1160
Qy	1586	GACCATATGAGAGGAGTGGTTTCATCAGAGTGTGCGACAGAACTCCACATCAAAAGGTGCTTTC	1645
Db	1161	GACTTACGTGGAGGTGGTTCATCAATAGTGTGGCCCAAACTCCACTCMAAAGGTGCTTCC	1220
Qy	1646	CTTCACCAACACGACCCCTGGAGACATCCTGAATCTCTTCTGACGTACGTCTATCCG	1705
Db	1221	CTTCACCAACACGACCCCTGGAGACATCCTGAATCTCTTCTGACGTACGTCTATCCG	1280
Qy	1706	CGTGGCCAGCGGCTACTTCTCATGATGTGCGATATGGCTGTCTAACCATGGTGGCGTGGGA	1765
Db	1281	AGTGGCCAGCGGCTACTTCTCATGATGTGCGATATGGCTGTCTAACCATGGTGGCGTGGGA	1340
Qy	1766	CTGCTCCAAAGTCCACAGGTGCGGTGGGGGTGCGTGGCGTCTGCTGGTGGCTACTGTCACT	1825
Db	1341	CTGCTCCAAAGTCCACAGGTGCGGTGGGGGTGCGTGGCGTCTGCTGGTGGCTACTGTCACT	1400
Qy	1826	GGCTCTCAGGACAGCGGCTGTGCTCATGTGATGCGAATTTCTCTTAACAGCTCAGCAACTCA	1885
Db	1401	GGCTCTCAGGATTTGGGCTGTGCTGTCTGCTGATGGCAATTTCTTTAAATGCTCAGCAACTCA	1460
Qy	1886	GGTTTTGGCATTTCTCGCTCTTGTTGGTTGGTGGATGATGATTTTTCTTCTGGCCCAAGC	1945
Db	1461	GGTTTTGGCGTTTCTTGCTCTTGTTGGTTGGTGGATGATGATTTTTCTTCTGGCCCAAGC	1520
Qy	1946	CTTTCACAGAAACAGACACAAATATAAAGAAATCCCTTTTGGAGGACAGACCGGGGAGTGGCT	2005
Db	1521	ATTTCAGTGAATAACAGGACAAATATAAGAGATTCATTTTGGAGACAGACTGGGAGTGGCT	1580
Qy	2006	GAAAGCGACAGAGGCGCAGGTGGCCCTCAGCTCATCAGAAATGTCACAGCTCTCTCAT	2065
Db	1581	CAGAAGCACCGGAGCGCAGGTGGCCCTCAGCTCATCAGAAATGTCACAGCTCTCTCAT	1640
Qy	2066	GGCCGCGTTAATCCCAATTCGCGCTCTCGGGGCGTTCCTCTCCAGGACAGCGGTAGT	2125
Db	1641	GGCCGCGATTATCCTCATCTCCTGCGGAGGCGTTCCTCTCCAGGACAGCGGTAGT	1700
Qy	2126	GGGTTCATATTTTTGCCATGTTCTGTCATTTTTTCGCGAAATTTCTCGAATGATTTATA	2185
Db	1701	GGATTCATATTTTGGCATGTTCTGCTCATTTTTCTCGCAATTTCTAGCATTGATTTATA	1760
Qy	2186	TCGACGCGAGAGACAGGAGATGATTTTTCTGCTGTTTACAAGCCCTGCGCTCAGAG	2245
Db	1761	CAGACTGAGAGACAGAAGATTTGATTTTTCTGCTGTTTACAAGCCCTGCGCTCAGAG	1820
Qy	2246	AGTGATTCAGTTGAACCTTAGGCCCTACACCGACACACAGACAAATACCGGCTACAGCC	2305
Db	1821	GGTGATTCAGTTGAACCTTAGGCCCTACACCGACACAGACAAATACCGGCTACAGCC	1880
Qy	2306	CCCACTCTCCCTTACAGGACACAGCTTTGGCCATGAAACCGAGATTTACATGACGTCCAC	2365
Db	1881	CCCACTCCCATATACAGGACACAGCTTTGGCCATGAAACCGATATCACTATGACGTCCAC	1940
Qy	2366	TGTTCACGCTCCGACGAGATGAGACCCCAACAGCGACGTGTACTACACACACGCTGAGCC	2425
Db	1941	CGTTTCAGCTCCGACAGAGATATACCTCTCACAGCGACGTGTACTACACACACGCTGAGCC	2000
Qy	2426	GGGCTCCGAGATCTGTGTGAGGCGGTACCGGACCGGACAGACAGACCCCTGAGTCCAGAG	2485
Db	2001	AGGCTTGAATTTCTGTACAGCTGTGTACCGTACCCCAAGACAACTCTGAGCTGTAGAG	2060
Qy	2486	CCCAGAGACACACAGCTCCACAAGGACACGTCTCCACAGTTCTCCGACTCCAGCTCCACA	2545
Db	2061	TCCCGAGAGACACAGCTCTACAGGGGACGTCTCTCCAGATTTCTCAGACTCTCAGCTTCA	2120
Qy	2546	CTGCTCTCAGAGCCCCCTGTACGAAGGTGAGACACTCATCTTTTGTGTAGAAAGCATATGCG	2605
Db	2121	CTGCTCTCAGAGCCCCCTGTGACCAAGGTGAGACACTCTCTCTTTGTGCAAGAAAGCATATGCG	2180

QY	2606	TCCTTTTCCTCTGTAAGCAAAAGGCAAGGAGTAGTGGATCTTCCTTTTTCGTGGCCCTTGGCT	2666
Db	2181	TCCTTTTCCTCTGTAAGCAAAAGGCAAGGAGTAGTGGATCTTCCTTTTTCGTGGCCCTTGGCT	2240
QY	2666	GGGGGCTCAAGCCCTTATTATGGCACCACCCGAGGTGAGAGACGGGGCTTGAGCCTTAACGGACATTTGT	2725
Db	2241	GGGGGCTCAAGCCCTTATTATGGGACCACCCGAGGTGAGAGACGGGGCTTGAGCCTTAACGGACATTTGT	2300
QY	2726	ACCTGGGGAAACACAGAGATTATGACTTTATTGCTGGACATTTCAATFACTTTCTTCTTCTA	2785
Db	2301	TCCCGGGGAAACACAGAGATTATGACTTTATGCTGGCCAGTTCCAGTACTTCTCTTTCTA	2360
QY	2786	CACATGTATATATAGTCACCCAGAAAGACACACTTACCCGAATATCCAGCAGCTTACTTTTACGA	2845
Db	2361	CACATGTATATATATAGTCACCCAGAAAGACACACTTACCCGAATATCCAGCAGCTTACTTTTACGA	2420
QY	2846	CCTACACAGAGAGTTTCAGTAACTGATGATGTGTCATGTTTGGAAAGAAACAACAGCTTCC	2905
Db	2421	CCTATATATAGAGATTTTCAGCAATGTGAAGTATGTCAATGCTGGACAGACAACAGCAACTTCC	2480
QY	2906	CAAAATGTGGCTGCAGCTACTTCTTGAGACAGTGGCTTCAGGGGAGCTTCAGAGATCATTTTGCAG	2965
Db	2481	CCAAATGTGGCTGCAGCTACTTTCATGAGACTTGCCTTCAAGAGCTTCAGAGATCATTTTGCAG	2540
QY	2966	TGACCTGGGAAACCCGGGAAATCATGCCAAAACAATTTACAAAGATGATCAGACGATGGAGT	3025
Db	2541	TGACCTGGGAAACCTGGGAGAGATCATGCCAAAACAATTTTAAATAATGATCAAGATGACGGGGT	2600
QY	3026	CCTTTGCGCTTACAAACCTCTCTGGTGGTGAACCCGGCACCCCGGAGTAACGCCATGCAACNTACGCC	3085
Db	2601	CCTGCGCTTACAAACCTCTCTGGTGGTGAAGCTGGCACCCGAGACAAACCCCATGCAATTAATCA	2680
QY	3086	GTTTGACTTAACAGAGCGTCTGGTGGATCAGATGTGCATCATTAATCCAGCCCTTCTTCAT	3145
Db	2661	GTTTGACTTAACAGAGCGTCTGGTGGATGAGCGAATGTGCATCATTAATTCGAGCGCTTCTTCAT	2720
QY	3146	CTAAGCTGACGGCTTTGGGTCACAGACAGACCCCGTCGCTATGCTGCTTCCAGGCCAATCAT	3205
Db	2721	CTAAGCTGACGGCTTTGGGTCAGCAGACAGACCCCTGTATGCTTACGTGCTTCCAGGCCAATCAT	2780
QY	3206	CCGGCCACACCCGACAGAAATGGGTTCCACGACAAAGCCGATACATGCGCTCAAAACAGAGCT	3265
Db	2781	CCGGCCCTCACCCGCGGAGTGGTTCATGTACAAAGCCGATACATGCGCAGAGACAGACAGCT	2840
QY	3266	GAGAAATCCGGCAGCAGAGAGCCCATGTAGTATGCGCCAGTTCCCTTCTTACTCTCAACGGGTT	3325
Db	2841	GAGAAATCCCGAGCAGAGAGCCCATGTAGTATGCGCTTCAAGTTCCCTTCTTACTCTCAACGGGCT	2900
QY	3326	GGGGGACACCTCAGACTTTTGTGGAGCAATTGAAAAAGTAAAGCACTTTCGACCACTA	3385
Db	2901	ACGAGACACCTCAGACTTTTGTGGAGCAATGAAAAAGTAAAGCACTTTCGTAACAACCTA	2960
QY	3386	TACGAGACCTTGGGGCTTCCAGTTTACCCCAACGGCTACCCCTCTCTTCTTGGAGAGCAGTA	3445
Db	2961	TACGAGACCTTGGGAGCTTCCAGCTTACCCCAATGGCTTACCCTCTCTGTCTTGGAGAGCAGTA	3020
QY	3446	CATGGGCTTCGGCAGCTGGCTGCTGCTGTTCATCAGCGTGGTGTGGGCTGCGACATTCT	3505
Db	3021	CATTCACCTTCGGCAGCTGGCTGCTGTGTATCATCAGCGTGGCTGCTGCGACAGTTTCT	3080
QY	3506	CGTGTGCGGTGCTTCTCTTGTGAACCCCTGAGAGGGCCGGGATCATTTGTATGGGCTGGGC	3565
Db	3081	AGTGTGCGAGTCTTCTCTCTGTAACCCCTGAGAGGGCCGGGATCATTTTGTATGGGCTGGGC	3140
QY	3566	GCTGATGAGCGTTCAGCTGTTCCGCAATGATGGGCGTTCATCGAATCAAGCTCACTGGCGT	3625
Db	3141	TCGTGATGAGCGTTCAGCTGTTTGGCATGATGGGCGTTCATTGGGATCAAGCTGAAGTGGCTGT	3200
QY	3626	GCCCGTGTGATCTGATGCTTCTGTGTGGCATAGAGAGTGGAGTTCACCGTTCACGTTGC	3685
Db	3201	GCCCTGTGTGATCTGATGCTTCTGTGTGGCATCTGTGGCATCTGGAGTGGAGTTCACCGTTCACGTTGC	3260

OY	3686	TTTTGGCCCTTTCAGACGGCCTCGGCCACAGAACCGGAGGGCTGTGCTTGCCCTGGAGCA	3745
Dp	3261	TTTTGGCCCTTTCAGACGCATTGGGACACAGAACACAGGGCTATGCTTCGCTTGGAGCA	3320
OY	3746	CATGTTTGCACCCGCTCTGGATGGGCCCGCTGCACCTCTGCTGGAGTCTGTATGCTGGC	3805
Dp	3321	CATGTTTGTCTCCGCTTCTGGACGGCTGTGCTGCACCTCTGCTGGTACTGATGCTTGC	3380
OY	3806	GGGATCTGAGTTTGCATCTTCACTTATGTCAGATATTTCTTGTGCTGTGGCAATCCACCAT	3865
Dp	3381	AGGGTCCGAAATTTGATTTATTTATGTCAGATATCTTTGGCCGCTGGCAATTCACACGT	3440
OY	3866	CCCTGGCCCTTCTCAATGGGCTGGTTTGGCTTCCCGTCTTTGCTCTTTGTTGGACATA	3925
Dp	3441	CTTTGGGGGTTCCTCAATGAGCATGTTCTGCGTCCGTGTCCTTATCTTTTGGACCGTG	3500
OY	3926	TCTCTGAGTGTCTCCAGCCACGGCTTGAACCGCCCTGGCCACACCCCTCCCTGAGCCAC	3985
Dp	3501	TCTCTGAGTGTCTCCAGCCCAATGGCTTAAACCCACACTGCCACATCTTCGCTTGAGCCGC	3560
OY	3986	CCCCACCGTGTGTCGGTCTGGCCATGTGCGCCCGCCGACAGCCACAGGGGTCATGTCCTC	4045
Dp	3561	TCCAACTGTGTCGGTCTGGTTCGCTGCTGCTCTCTGTGTACACCAACAAATGGGTGATTCCTC	3620
OY	4046	CGACTCGAGTATAGTTTCCAGACGACAGTGTCAAGCCCTCAGCGAGAGGTTTGGCCTA	4105
Dp	3621	CGACTCGAGTATACAGCTCTCAGACCAACGGGTCTGGCATCAGTAGAGTCCAGGCAATA	3680
OY	4106	CGAGGCCCGCAGAGGGCGGGAGGCCCTGCCACCAAGTATGTGTGAACCCACAGAAAA	4165
Dp	3681	CGAAGCAGACGAGGGGTCCGGAGGCCCTGCCACCAAGTATGTGTGAACCCACAGAAAA	3740
OY	4166	CCCGCTCTTTCGCGCCACTGTCACACTGTGTGCTCCATCCCGAATCCAGGCAATACCACCCCTTGAA	4225
Dp	3741	CCCTGCTTTTGGCCCGGGTCCACATGTGTTCATCCGGATCCAGACATCAGGCTCCCTTGAC	3800
OY	4226	CCCGAGACAGCAGCCCACTGGACTCAGGGTCTCTGCTCTCCCGAGCGCAGAGCCACGA	4285
Dp	3801	CCCTGGGCAACAGCCCACTGGACTGACTGCTCTGCTCTCCCGAGCGCAGAGCCACGA	3860
OY	4286	GGCCCGCAGAGCCCCCCCCAGAGAAAGCTGTGGCCACCCCTCTACAGACCGGGCGAGGA	4345
Dp	3861	GGCTGAGAGGATCCCCCTTAGAGAAAGGCTTGGCGCCACCCCTACAGACCGGCGAGGA	3920
OY	4346	CGCTTTTGAATTTTCTACTGAAGGGCAATCTGGCCCTAGCAATAGGGCCCGCTGGGGCCC	4405
Dp	3921	CGCTTTTGAATTTTCTACTGAAGGGCAATCTGGCCCTAGCAATAGGGACCGCTGAGGGCC	3980
OY	4406	TGCGGGGGCGCGCTTCTCANAAACCTTGGAACCCAGGCTGCACATGCCATGGGAGCTCCGT	4465
Dp	3981	CGGTGGGGCGCGCTTCTCANAAACCTTGGAACCCAGGCTGCACACCGCATGGGAGCTCTGT	4040
OY	4466	GCCCGGCTACTCCAGCCCACTACACACTGTGAGCGGCTCTGCGCTTCGCTGACTGCGCGCT	4525
Dp	4041	GCCCGGCTACTCCAGCCCACTACACACTGTGAGCGGCTTCTGCTCGGTGACTGTTGCTGT	4100
OY	4526	GCACCCGCCCGCTGTTCCTCGGGCCTGGCGGAACCCCCGAGGGGCACTGTGCCAG---	4581
Dp	4101	GCATCCCCCGCTG-----GACCTGGGGCGCAACCCCCGAGGGGGCGCCCTGCAGGCTA	4154
OY	4582	-----GCTAACCTGAGACTGACCGGCGCTGTTTGGAGACCCCAAGTGGCTTTCCAGCT	4636
Dp	4155	TGAGAGCTAACCTGAGACTGATCAGCGGGATATTTTGGAGATTCCTCAATGTGCTTTTATGT	4214
OY	4637	CCGGTGTGAGAGAGGAGATTCGAAGGTGGAAGTCATTTGAGCTGCAGAGAGTGTGAATGCGA	4696
Dp	4215	CAGGTGTGAGAGAGGAGATTCGAAGGTGGAAGTCATGAGAGCTACAGAGAGTGAATGTGA	4274
OY	4697	GGAGAGGCCCGGGGAGAGAGCTCCAACTGA	4727
Dp	4275	GGAGAGGCCCGGTGGGAGAGCTCCAACTGA	4305

[illegible]



D	b		2	GACCGGCGGGCAGCAATGTCCTCGGCCCTTACGCCTTTAGACC	C	GGAACCCGAGAACCGGCA	61
O	y	427	GGCGGCGACGCGCTGTATCGTGCC--CGGGAGCGCGCGTGAAGCGGAGCGCA	483			
D	b	62	GCACCGCGGGCGCGCACGCCGTTTCGGCGGAGAGATGCCCGCGCGCGCG	121			
O	y	484	GACGCAACGGGGGGCTGCCCCGTGCTGCCGCGCGGACCGGGACTATCTGCACCGGCCA	543			
D	b	122	GGCGGAGCGGAGGACCCCGCGCGCGCGCGCGCGCGGAGTAATCTCAGCGGCGGA	181			
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O	y	724	TGGATTAAGAGCGAACCCTCGAACCAACGTGGAGAGCGTGGGTGGAGTTGGAG	783			
D	b	359	TGGGATACCGGGCGCAACTTAGAACCACTTAGGAGCGTGGGTGGAGTTGGAG	418			
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D	b	419	GACGAGTAAGTGTGAGATTAACTACACACGAGAAAGATTGAGAGAGGCTATGTTA	478			
O	y	844	ATCCTCACTCATGATACAGACCCCTTAAGAGAGAGGTCTAATGTCTGACCAAGAG	903			
D	b	479	ACCCCGCTCATGATTCAGACTCCACAGGAMATGGAATTAATGTACTCAACAAGAG	538			
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O	y	1204	AAGTGAACAGCTGCGGAGAAATGCTGAATTAAGGCTGAGGTTGCTCATGTATATGAGC	1263			
D	b	839	AAGTGAAGAGCTGCGGAGAAATGCTGAATTAAGCAAGAGGTTGGTATGTTATATGATC	898			
O	y	1264	GGCCCTGCTCAATCCGGCGGATCCAGACTCGCCCGCCACAGCCCCCAACAAAAATTC	1323			
D	b	899	GACCTTGGCTTAATCTGTGATCTTGATTTGCCAATCAACAGGTCCCAATAAATTTCTA	958			
O	y	1324	CCAAACCTTTATATATGAGGCTTGTGTTGATATGATGATGATCAATGCTTATCCAGAA	1383			
D	b	1019	ACATGATTTGGAGGAAGATTAATATATATGATGATGATCAAGAAACAGTTCTGGTAA	1078			
O	y	1444	TGCTGACGCGCATGCCCTGCGAGACCATGTTCCAGTTAATGACTCCCAAGCAATGTAC	1503			
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[illegible]







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VERSION AF119569.1 GI:4325110  
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SOURCE human.  
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REFERENCE 1 (bases 1 to 3453)  
Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and  
Tollgard,R.  
PTCH2, a novel human patched gene, undergoing alternative splicing  
and up-regulated in basal cell carcinomas  
JOURNAL Cancer Res. 59 (4), 787-792 (1999)  
MEDLINE 99151521  
AUTHORS Zaphiropoulos,P.G., Unden,A.B., Rahnama,F., Hollingsworth,R.E. and  
Tollgard,R.  
TITLE Direct Submission  
JOURNAL Submitted (12-JAN-1999) Bioscience, Karolinska, Huddinge 141 57,  
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ORGANISM	Mus musculus			
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AUTHORS	Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
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JOURNAL	Takabatake,T			
Direct Submission				
Submitted (04-FEB-1998)				
to the DBJ/EMBL/GenBank databases.				
Takabatake, Nagoya University, Radioisotope Research Center;				
Furo-cho, Chikusa, Nagoya, Aichi 464-8602, Japan				
(E-mail:145998a@nuc.cc.nagoya-u.ac.jp, Tel:052-789-2573,				
Fax:052-789-2567)				
2 (sites)				
Takabatake,T., Ogawa,M., Takahashi,T.C., Mizuno,M., Okamoto,M. and				
Takeshima,K.				
Hedgehog and patched gene expression in adult ocular tissues				
FEBS Lett. 410 (2-3), 485-489 (1997)				
3 (sites)				
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Motoyama,J., Takabatake,T., Takeshima,K. and Hui,C.-C.				
pitch2, a second mouse patched gene is co-expressed with Sonic				
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Nature Genet. 18, 104-106 (1998)				
On Feb 6, 1998 this sequence version replaced gi:2598660.				
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ORIGIN

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DB 379 CTGACACAGAGAAGGCTCTCTACAAACCTGGACTCGGCACTCCAGGCGACGCTGTCCAT 950
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Matches 1097; Conservative 0; Mismatches 4; Indels 519; Gaps 1;

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QY 4188 GTGGTCATCCGCAATCCAGCATCACCCCTCGAAACCCGAGACAGCCCACTG 4247
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QY 4248 GACTCAGAGTCCTCCCTCCCGGAGCGCAAGCCAGCCCGGAGAGACCCCCCA 4307
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Db 131544 GAAGGCTTGTGGCCACCCCTTACAGACCGGAGAGAGCGTTTGAANAATTTCTAGTA 131485

QY 4368 GGGCATTTCTGGCCCTTACCAATAGGGCCCGCTGGGGCCCTCGCGGGGCCCTTCTCAAC 4427
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Db 131484 GGGCATTTCTGGCCCTTACCAATAGGGCCCGCTGGGGCCCTCGCGGGGCCCTTCTCAAC 131425

QY 4428 CTTGGAAACCCAGCGTCACACTGCGGAGGAGCTCCGTCGCCGCTACTGCCAGCCATC 4487
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Db 131424 CTTGGAAACCCAGCGTCACACTGCGGAGGAGCTCCGTCGCCGCTACTGCCAGCCATC 131365

QY 4488 ACCACTGTGAGCGGCTTGTGCTCGTGAAGCTGTCGCGCGTGAACCCCGCTGTCCCTGG 4547
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Db 131364 ACCACTGTGAGCGGCTTGTGCTCGTGAAGCTGTCGCGCGTGAACCCCGCTGTCCCTGG 131305

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QY 4809 CTGTTGAGCTATGGAAGAGATGCCCTGTGCGAGAGACAGTTCATTGTACTGTAAAC 4868
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QY 4869 CGATTGATTAATTTGTTAAATATTTCTATTAATTTAAGAGATGTACATGTGTAAAT 4928
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QY 4929 ATAGGAAGAGAGATGTAAAGTGTATGATCTGGGGCTTTCACACCTGCGCCAGAGTG 4988
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QY 5229 AACAGCTATGCGTGAATTTTGTGTTTAAATGAGAGATATGAAAGAGCCCGGAATT 5288
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Search completed: January 13, 2001, 09:21:32  
 Job time: 11240 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:17:42 ; Search time 217.09 Seconds

(without alignments)  
9150.602 Million cell updates/sec

Title: US-08-656-055-18

Perfect score: 5288  
Sequence: 1 GAATTCGGCGGACCGCAAG.....TATGAAGAAAGCCCGAATT 5288

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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22: /cgn2\_2/gcgdata/geneseq/geneseqn/NA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5288	100.0	5288	17 T14220	Human patched gene
2	5288	100.0	5288	20 V64093	Human patched gene
3	5281.6	99.9	5288	19 V21590	Human patched gene
4	4684.8	88.6	6568	19 V15949	Human patched gene
5	3801.2	71.9	5187	19 V21587	Human patched gene
6	3801.2	71.9	5187	20 V64092	Human patched gene
7	3801.2	71.9	5187	20 V64099	Human patched gene
8	3798.4	71.8	5187	19 V21589	Human patched gene
9	3778	71.4	5187	17 T14218	Human patched gene
10	1176.4	22.2	4030	20 Z31717	Human patched-2 co
11	1173.2	22.2	4391	20 X89478	Human patched-2 co
12	1171.6	22.2	3453	21 A09081	Human patched-like

13	593.8	11.2	2082	20 Z31729	Human patched-2 co
14	472.2	8.9	1734	19 V15998	NBCS (PTC) protei
15	433.8	8.2	2032	19 V69382	Human patched-2 cd
16	427.2	8.1	445	20 V87142	EST clone BL160.
17	411.8	7.8	3900	16 O91660	Drosophila patched
18	405	7.7	4434	20 V64100	Drosophila melanog
19	228	4.3	228	20 Z31719	Human patched codi
20	183.6	3.5	4004	20 Z31728	Human patched-2 co
21	137	2.6	12886	21 A09084	Human patched-like
22	132	2.5	228	20 Z31718	Human patched codi
23	85	1.6	114955	20 X53491	Human adenosine A1
24	77.8	1.5	114955	20 X53491	Human adenosine A1
25	77	1.5	345	17 T14224	Mosquito patched g
26	77	1.5	345	19 V21588	Anopheles gambiae
27	77	1.5	345	20 V64101	Anopheles gambiae
28	76.6	1.4	4550	20 X06873	Human NPC1 cDNA (N
29	74.2	1.4	477	21 Z44307	Human SCA7 genomic
30	73.4	1.4	5029	20 X06874	Mouse NPC1 gene or
31	70.4	1.3	138	19 V69383	Human patched-2 ES
32	69.2	1.3	1272	20 X09010	Brn-3a polynucleot
33	69.2	1.3	4020	18 T91361	Orf virus genomic
34	69.2	1.3	4524	20 V33912	Nucleotide sequenc
35	68.4	1.3	126	21 A09082	Human patched-like
36	67.2	1.3	3946	18 T93610	Mycobacterium tube
37	66.6	1.3	736	17 T14225	Battle patched gen
38	66.6	1.3	736	19 V21586	Tribolium castaneu
39	66.6	1.3	736	20 V64098	M. tuberculosis im
40	65.6	1.2	1439	19 V64533	M. tuberculosis im
41	65.6	1.2	1439	19 V44424	M. tuberculosis im
42	65.6	1.2	1439	20 Z19334	M. tuberculosis an
43	65.6	1.2	1439	20 Z19122	M. tuberculosis re
44	65.6	1.2	1439	20 Z19122	Cardiac adenyllyl c
45	65.4	1.2	334	20 V89418	EST clone CN552.

#### ALIGNMENTS

RESULT 1	
T14220	
ID T14220 standard; cDNA; 5288 BP.	
XX AC T14220;	
XX AC T14220;	
DT 30-JUL-1996 (first entry)	
XX DE Human patched gene.	
XX KW Patched gene; ptc gene; embryo development; cellular regulation;	
KW signal transduction; ligand; antibody; hedgehog protein;	
KW gene therapy; ss.	
XX OS Homo sapiens.	
XX OS Homo sapiens.	
FH Key	Location/Qualifiers
FT CDS	384..1427
FT	/*tag= a
XX	
PN W09611260-A1.	
XX	
PD 18-APR-1996.	
XX	
PF 06-OCT-1995; 95WO-US13233.	
XX	
PR 07-OCT-1994; 94US-0319745.	
XX	
PA (STRD ) UNIV LELAND STANFORD JUNIOR.	
XX	
PI Goodrich LV, Johnson RL, Scott MP;	
XX	
DR WPI: 1996-209842/21.	
XX	
DR P-PSDB; R75375.	
XX	

PT DNA encoding patched protein other than Drosophila patched protein -  
 PT used to produce antibodies which detect or inhibit patched protein  
 PT ligand signal transduction in cells

Example: Page 53-56; 70pp; English.

CC A cDNA clone (T14220) coding for the human patched protein (PTC)  
 CC (R75375) was obtd. by screening a human lung cDNA library with a  
 CC 1 kb portion of the mouse ptc gene (see also T14218) and examination  
 CC of isolated clones. The human ptc gene has about 89% identity to  
 CC the mouse ptc gene. The 5' and 3' untranslated sequences are highly  
 CC similar to mouse ptc, suggesting conservation of regulatory  
 CC sequences. The human ptc gene can be used for prodn. of large  
 CC amounts of recombinant PTC, as a probe e.g. to detect gene  
 CC mutations, in gene therapy, to study embryo development, to produce  
 CC transgenic animal models, etc.

Sequence 5288 BP; 1182 A; 1530 C; 1417 G; 1159 T; 0 other;

Query Match 100.0%; Score 5288; DB 17; Length 5288;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGGGACCGCAAGAGTCCCGGAGACGCCCGGAGACAGAGCTCCTCGGCGC 60  
 Db 1 gaattccgggggacccgaagagtgcccggaagcccggaagacagagctcgcgcgc 60  
 QY 61 GCCGGCTCTCGCTTCCTCCGCAACTGTGATGTGGGACAGCGCGCGCGAGACCTCGGGA 120  
 Db 61 gccggctctcgccttcctccgcgaacttgatgtggacagcgcgccgagagactcggga 120  
 QY 121 CCCCCCGCAATGTGGCAATGGAAGGCGCAGGCTTGACTTCCCGGCGAGCGCGCGCC 180  
 Db 121 ccccccgcaatgtggcaatggaaaggcgaggtctgactcccgagcgcgcgcc 180  
 QY 181 GCAGGCGGACGACGCGCGCGCGGTGTGAGACGACGAGCGCGGTGTGTAAACCGAGGCC 240  
 Db 181 gcaggcggacgacgcgcgcgcggtgtgagacgacgagcggtgtgttaaccgaggcc 240  
 QY 241 CGAGCGCGACGACCTGCGCGCGACGAGCGCTCTCGCAAGCGGCGCGCGCGCGCGCGC 300  
 Db 241 cgagcgcgacgacctgcgcgcgacgagcgctctcgcaagcgcgcgcgcgcgcgcg 300  
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 Db 301 cagcgcggacgacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 360  
 QY 361 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 420  
 Db 361 gcggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 420  
 QY 421 GCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 480  
 Db 421 gcggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 480  
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 Db 481 gcagcggacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 540  
 QY 541 CCAGTACTGCGAGCGCGCGCTGCTGCTGTGAGACAGATTTCGAAGGGGAGGCTACTGGCC 600  
 Db 541 ccagtactgcgagcgcgcgctgctgctgtgagacagatttcgaaggaggctactggcc 600  
 QY 601 GGAAGCGCCACTGTGCTGAGAGCGAAGTTTCAGAGACTTAAATTAACCTGGTGGT 660  
 Db 601 ggaagcgccactgtgctgagagcgaaagtttcagagactttaattaacctgggtgg 660  
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 Db 661 acattcaaaaaaagtggcgcaagttcttggtgtgggctctcatatttgggcgcttgg 720  
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Db 721 cgttgagattaaagcaggaacctcgagacacagctggagagctgtggtgaggttg 780  
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QY 3061 GCGATTAAGCCCATCGACATCCAGCTTACCTAAACAGGCTGTGGTAGATGATGATGCA 3120  
Db 3061 gcgataagcccatcgacatcagccagcttgacataaagcgtcgtgtgagatcgagatgga 3120  
QY 3121 TCATTAATCCAGCGCTTTCTTACATCTACCTGACAGGCTTTGGGTGACCAACGACCCCTGC 3180  
Db 3121 tcattaatccagcgcttcttcaatctactcagccttgagcgtctgtgtgcagaaagaccgtctg 3180  
QY 3181 CGTATGCTGCTCCAGGCAACATCCGGCCACACCCAGACCAATGGGTCCACGACAAG 3240  
Db 3181 cgtatgctgctcccgagcccaacatccggtccaacaccgacagatggtctcacgacaaag 3240  
QY 3241 CCGACTACATGCTGAAACAAGGCTGAGAAATCCCGGACAGAGCCCATGAGTATGCCC 3300  
Db 3241 ccgactacatgctgaaacaagcctgagaaatcccgacagagcccatcgagatagccc 3300  
QY 3301 AGTTCCCTTTTACCTCAACGGGTTGCGGGACACCTCAGACTTTGTGAGGCAATTGAAA 3360  
Db 3301 agttcccttctactcaacaggtgtgcggtgaacccctcagacttgtgtgaggtgaattgaaa 3360  
QY 3361 AAGTAAGACCATCTGACAGCAACTATACGACCTTGGGGCTGTCCAGTTACCCCAACGGCT 3420  
Db 3361 aagtaagaccatctcgcagcaactatacagccttgggtgtgtcagattaccccaagcgtc 3420  
QY 3421 ACCCTTCCTCTTCTGGGAGCAATGAGGCTCCGCCACTGGCTGCTCTGATCA 3480  
Db 3421 acccttctctctctcggagagcagatcacatccgcgtccgcacatggtcgtgtgttca 3480  
QY 3481 GCGTGTGTGGCTGACATTCCTGCTGTGGCTGTCTTCTGAAACCCCTGAGAGG 3540  
Db 3481 gcgtgtgtgtgcctgcacattcctgctgtgtgcgtgtcttctctcctcgaacccctgtgcg 3540  
QY 3541 CCGGGATATATGTGATGATGCTCTGCGGCTGATGACGCTCGAGCTGTGGCATATGGGCC 3600  
Db 3541 cccggatataatgtgatatgtctcctgagcgtgatatgacgctcgagctgtggcatatgggcc 3600  
QY 3601 TCATCGGAATCAAGCTCAAGTGGCGGCTGCGCTGATGCTGATGCTGCTGTTGGGCTAG 3660  
Db 3601 tcacggaatacaagctcaagctgtgcgtgtgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3660  
QY 3661 GAGTGAAGTTACCGTTGACGTTGCTTGGCTTCTGACGGGCCATCGGGACAGAAAC 3720  
Db 3661 gagtgaagttcacacgtctcaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3720  
QY 3721 GCAGGGCTGTGCTTCCCTGAGGACATGTTTGACACCCGCTCTGTGATGGCGGCTGTGCA 3780  
Db 3721 gcagggctgtgcttccctgagacatglttgacacccgtctgtgagctgtgcgtgtgtca 3780  
QY 3781 CTTGTGCTGGAGTGTGATGCTGAGGCGGAGTTCAGTTCGACTTCATGTCAGGTATTTCT 3840  
Db 3781 ctctgtcgtggagtgctgtagtctgtgcggagatccgaagttcgaactcatctgttcaagttatct 3840  
QY 3841 TTGCTGTGCTGGCAATCTCACACATCTGGGGTTCTCAATGGGCTGTGTTTCTTCCG 3900  
Db 3841 ttgctgtgctggcagtctcaccatccatccctgcgtgtctcaatgtgtgtgtgtgtgtgtgtgt 3900  
QY 3901 TGTCTTTGTCTTTCTTTGGACATATCTCTGAGAGTGTCTCAGCAACGGCTTAACCGCC 3960  
Db 3901 tgtcttctgtcttctcttggacatactccctgaaggtgtcttccaaacagcgttgaacccgc 3960  
QY 3961 TGCCCAACCCCTCCCTTACGCAACCCCGCAGGCTGTGCGCTTCGCAATGCGCCCGCGCC 4020  
Db 3961 tgcccaacccctcccttgaagcaaccccccaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 4020

QY 4021 ACAGCAGCAGCGGCTGATTCCTCCGACTCGAGATATGTTCCAGACAGATGTCAG 4080  
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 Db 4021 acagcacagcggtctgattctctccgactcgaglatagtlcccaagacagtgltcag 4080  
 QY 4081 GCGTCAGGAGAGAGCTTGGGCACTACGAGGCCAGAGGGCGGGAGGCGCTGCCACC 4140  
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 Db 4081 gcttcagagagagcttcgacatacagagcccaagagggcggagggccctgcacac 4140  
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 Db 4141 aagtgatctgtagaacacacagaaaccccgcttcgcccactccacttgcgtccatcccg 4200  
 QY 4201 AATCCAGGCATCACCCACCTTCGAACCCGAGACAGACGCCACCTGACTCGAGTCCC 4260  
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 Db 4201 aatccaggtatcacccacttcgaacccgagacagagcccaactgcgactcagggltccc 4260  
 QY 4261 TGCTCCCGGAGCGCAAGGCCAGAGCCCCGAGAGACCCCGCCAGAGAAAGGTTGTGGC 4320  
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 QY 4321 CACCCCTCTACAGACCGCGCAGAGAGCGCTTTGAATTTCTACTGAAGGCAATTCGGCC 4380  
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 Db 4321 caccctctacagacccgacgagacgacttltgaaattctactgaaggtcattcgtggc 4380  
 QY 4381 CTAGCAATAGGCGCCGCTGGGGCCCTCCGGGGCCGTTCTGACAACCTCGGAACCCAG 4440  
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 QY 4441 CGTCACATGCGATGGGAGCGTCCGCGCGGCTACTGCGACGCCATCACACGTGTACGG 4500  
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 Db 4441 cgtccacgtcacaatggcgagctcgcgtgcgcgctacgtcagccacacacacgtgagcg 4500  
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 QY 4621 ACGTGCCCTTCGACGTCGGGTGTGAGAGAGGATTCGAGAGTGGAAGTATGACTGCTG 4680  
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 Db 4621 acgtgcctctccacgctccggtgtgagagagagatcgaaggtgagagatcgtgacgtgc 4680  
 QY 4681 AGGAGTGTGAATGCGAGGAGAGAGGCCCGGGGAGAGAGCTCAACTAGAGGTGTTAAAT 4740  
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 Db 4681 aggacgtgtgaatgctgagagagagagcccgggagagcagctccacatgagaggtatgaat 4740  
 QY 4741 CTGAAGCAAGAGGCCCAAGATGGAACCCGCCACCCCACTCTTTCAGAACTGCTT 4800  
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 Db 4741 ctgaagcagaagagcagaagatltgaaaccccccaactcttccagaactgctt 4800  
 QY 4801 GAGAGAACTGGTGTGATTTGAAAAGATGCTGTGCCAGAGAGATGTTGTTT 4860  
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 Db 4801 gaagagaaactgtgtgagatcgaagaaagatgcccgtgcaggaagatcattglt 4860  
 QY 4861 ACTGTAAACGATTTGATTTTGTAAATATTTCTAATAATTTTAAAGATGTGACACA 4920  
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 Db 4861 actgtaaacgactgtattatttgtttaaatttctataaattatataagagatgacaca 4920  
 QY 4921 TGTGTAAATATAGAAAGAGATGTAAAGTGTATGATCTGGGGCTTTCACACTCTGCC 4980  
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 Db 4921 tgtttaaataataggaagagatgtaaaggtgatactggggcttcccaactcctggc 4980  
 QY 4981 CCAGAGTGTGAGGCGCAAGTAGGGGCTCTCGTATTTGTGATGGGTGCTCGTGACACA 5040  
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 Db 4981 ccaagagtgagagcgcaagagtgaggccctccgtacttctgtgacatgaggtccgtgcaca 5040  
 QY 5041 ACCAAGCTTCAATAGTCTTAAATTTACACATATGTTGCTGCTTAAATATTTGTTAAT 5100  
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 QY 5101 TTACTTGTATATTTCTATGCAAAATATTTGCTTATGTAAATAGATTTATTTGTTAAAGGTTTC 5160

Db 5101 ttacttgataaatctcatgcaaatatgtcttatgataagatatttctgaaaggttcc 5160  
 QY 5161 TGTTTAAATATTTTAAATTTTGCATATCACAAACCTGTGGTAGTATGAAATGTTACTGTT 5220  
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 Db 5161 tgtttaaataattttaaatttgcatatacaacccctgtgtagatgaaatgttactgtt 5220  
 QY 5221 AACTTGAACACAGCTATGCGTGAATTTTGTGTTAATGAGCAGATATGAAGAAAGC 5280  
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 Db 5221 aacttcaaacacagctatggtgataatttltgtttaaagagacatatagaaagac 5280  
 QY 5281 CCGGAATT 5288  
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 Db 5281 ccggaatt 5288  
 RESULT 2  
 V64093  
 ID V64093 standard; cDNA; 5288 BP.  
 XX  
 AC V64093;  
 XX  
 DT 26-JAN-1999 (first entry)  
 XX  
 DE Human patched gene.  
 XX  
 KW Human: patched gene; diagnosis: treatment: developmental disorder;  
 KW cancer; healing: injured tissue: ptc; spina bifida; Wnt-1 oncogene;  
 KW sperm production; gene therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 384..4727  
 FT CDS /\*tag= a  
 XX  
 PN US5837538-A.  
 XX  
 PD 17-NOV-1998.  
 XX  
 PF 06-OCT-1995; 9505-0540406.  
 XX  
 PR 06-OCT-1995; 9505-0540406.  
 PR 07-OCT-1994; 9405-0319745.  
 XX  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Goodrich LV, Johnson RL, Scott MP;  
 DR WPI: 1999-023461/02.  
 DR P-PDB: W72969.  
 XX  
 PT Nucleic acid encoding vertebrate patched protein and related  
 PT transformants - used to express poly:peptide(s), useful for  
 PT diagnosis and treatment of developmental disorders or cancer, and in  
 PT healing of injured tissue  
 XX  
 PS Claim 1: Column 59-64; 38pp; English.  
 XX  
 CC The present sequence represents the human patched (ptc) gene. Cells  
 CC containing and expressing the ptc gene are used for the recombinant  
 CC production of the protein. These in turn are useful: (1) for generating  
 CC antibodies (Ab); and (11) to screen for specific-binding ligands  
 CC (potential therapeutic agonists and antagonists). The ptc gene, or its  
 CC fragments, are used to isolate related sequences from other mammals; to  
 CC identify mutations (particularly those associated with genetic diseases  
 CC such as spina bifida and other developmental disorders); to monitor  
 CC expression levels in testis (to determine relationship with sperm  
 CC production) and to isolate 5'-non-coding sequences (used to study  
 CC embryonic development and to provide regulated expression of proteins).  
 CC The complete gene can be used in gene therapy, including expression of  
 CC antisense molecules, and to generate transgenic animals for studies of  
 CC embryonic development. Ab are used diagnostically to determine the

CC p1c protein on cell surfaces and as competitive inhibitors of signal  
 CC transduction through the p1c ligand. Cells that have been engineered to  
 CC express the p1c protein can be used to promote regrowth and healing of  
 CC damaged tissue (e.g. growth of new teeth) and regulation of the p1c  
 CC protein expression may be useful in cancer treatment (it may control the  
 CC Mnt-1 oncogene).

XX Sequence 5288 BP: 1182 A; 1530 C; 1417 G; 1159 T; 0 other:

Query Match 100.0%; Score 5288; DB 20; Length 5288;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGGAGCCGCAAGAGTGGCCGGAGAGCCCGCAAGAGAGAGCTCGTCGCGC 60  
 Db 1 gaattccggggagccgcaagagtgccgcggaagcgccgaagagagagctcgtcgcgc 60  
 QY 61 GCGGCTCTGCTCTTCCGCAACTGATGTGGGCAAGCGGCGCGCAGAGACTCGGGA 120  
 Db 61 gccggctctgctcttccgcaactgatgtgggcaagcgcgcgccagagagactcggga 120  
 QY 121 CCCCCGCAATGTGGCAATGGAAGGCGCAGAGCTGATCCCGGACGCGCGCGCGC 180  
 Db 121 cccccgcaatgtggcaatggaaggcgcaagctgactcccgcaagcgcgcgccg 180  
 QY 181 GCACGCGCAGAGCGCCCGCCGCTGTGACGACGACGCGCGCTGTGTCAACCGAGCC 240  
 Db 181 gcacgcgcgagagcgcccgccgctgtgacgacgacgcgcgctgtgtcaacgagcc 240  
 QY 241 CGAGCCGAGAGCGCTGGGCGCAGAGGCTCTGCAAGCCGAGGCGCCAGCGCGCAG 300  
 Db 241 cgagccgagagcgctgggcgagagctctgcaagccgagcgccagcgcgcgccag 300  
 QY 301 GAGCCCGCAGCAGCGCGGACGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 360  
 Db 301 gagcccgagcagcgcgagcgagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 360  
 QY 361 GCGCGCGCGCGCGCGCGCGCAACATGGCTGTGGGTGATGAGCGCGCGCGCGCGC 420  
 Db 361 gcgcgcgcgcgcgcgcgcgcaacatggctgtgggtgatgagcgcgcgcgcgcgcg 420  
 QY 421 GCGCGCGCGCGCGCGCGCTGTATGGTCCCGGAGCGCGCGCGCTGTAGGCGGAGGC 480  
 Db 421 gcgcgcgcgcgcgcgcgctgtatgggtcccgagcgcgcgcgcgcgcgcgcgcgcg 480  
 QY 481 GCGAGCGAGCGGGGGGCTGCGCGCTGCGCGCGCGCGGACGAGCTATGCAACCGGC 540  
 Db 481 gcgagcgagcggggggctgcgcgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 540  
 QY 541 CGAGCTACCTGCGAGCGCGCGCTGCTGTGAGCAGATTTCCAAAGGGAGGCTACTGCC 600  
 Db 541 cgaactacctgagcgcgcgctgctgtgagcagatttccaaaggaggtactactgccc 600  
 QY 601 GGAAGCGCGCAGCTGTGCTGAGAGCGAAGTTTCAGAGACTTTATTTAACTGGGTTGT 660  
 Db 601 ggaagcgcgagctgtgctgagagcgaaagtttcagagactttatattaactgggtgt 660  
 QY 661 ACATTTAAAAAACTCGCGCAAGTTCTTGTTGGTGGCCCTTCATATTTGGGGCTTGC 720  
 Db 661 acatttaaaaaaactcgcgcaagttcttggttggtggcccttcattatctggggcttcg 720  
 QY 721 CGGTGGATTTAAAGCGCAACCTTGAGACCAAGTGGAGAGAGCTGTGGGTGCAAGTTG 780  
 Db 721 cgggtggatTTAAAGCGCAACCTTGAGACCAAGTGGAGAGAGCTGTGGGTGCAAGTTG 780  
 QY 781 GAGGAGAGAGTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
 Db 781 gaggagagagtggtgtaatttaatttaatttaatttaatttaatttaatttaattta 840  
 QY 841 TTTAATCTCAACTCAGATGATCAGACCCCTTAAGAGAGAGGCTTAATGTCTGACACAG 900  
 Db 841 ttaattctcaactcagatgatacagaccccttaagagagagtgcttaattcttgacacag 900

QY 901 AAGCGCTCTTACACACCTGAGCTCGAGACTCCAGGCCAGCGCTGCTCATGTATACATGT 960  
 Db 901 aagcgctcttTACACACCTGAGCTCGAGACTCCAGGCCAGCGCTGCTCATGTATACATGT 960  
 QY 961 ACAACAGGAGTGGAAATTTGGAAACATTTGTTTCAATAATCAGAGAGCTTATCAGAAA 1020  
 Db 961 acaacaggagtggaaatTTGGAAACATTTGTTTCAATAATCAGAGAGCTTATCAGAAA 1020  
 QY 1021 CAGGTTTACATGATCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080  
 Db 1021 caggTTTACATGATCAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080  
 QY 1081 ACTGCTTCTGGAGAGGCGGAAATTTACAGTGTGGAGACGCTACCTCTAGTAAACCTC 1140  
 Db 1081 actgcttctTGGAGAGGCGGAAATTTACAGTGTGGAGACGCTACCTCTAGTAAACCTC 1140  
 QY 1141 CTTTGGCGTGACAAACTTTCGACCCCTTGAATTCCTGGAAGAGTTAAAGAAATTAAC 1200  
 Db 1141 ctttggcgTGAACAAACTTTCGACCCCTTGAATTCCTGGAAGAGTTAAAGAAATTAAC 1200  
 QY 1201 ATCAAGTGAACAGCTGGGAGAGAAATGCTGAATTAAGGCTGAGCTTGTATGATACAT 1260  
 Db 1201 atcaagTGAACAGCTGGGAGAGAAATGCTGAATTAAGGCTGAGCTTGTATGATACAT 1260  
 QY 1261 ACCGCCCTGCTCAATCCGCGCGATCCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGC 1320  
 Db 1261 accgccctTCTCAATCCGCGCGATCCAGCTGCGCGCGCGCGCGCGCGCGCGCGCGC 1320  
 QY 1321 CAACCAAACTCTTTGATATGAGCCCTTGTGTAATGATGATGATGATGATGATGATG 1380  
 Db 1321 caaccaaactctTTGATATGAGCCCTTGTGTAATGATGATGATGATGATGATGATG 1380  
 QY 1381 AGTATATGACCTGGCAGAGAGAGTGAATGTTGGGTGTCACAGTGAAGACGCTGGAA 1440  
 Db 1381 agtatatGACCTGGCAGAGAGAGTGAATGTTGGGTGTCACAGTGAAGACGCTGGAA 1440  
 QY 1441 AACTGTCAGCGGCCATGCGCTGAGACCATGTTCCAGTTTATGATGATGATGATGATG 1500  
 Db 1441 aactgtcagCGGCCATGCGCTGAGACCATGTTCCAGTTTATGATGATGATGATGATG 1500  
 QY 1501 ACAGAGACTTCAAGGGGTACGAGTATGCTGCACATCAATCAATCAATCAATCAATCA 1560  
 Db 1501 acagagactTCAAGGGGTACGAGTATGCTGCACATCAATCAATCAATCAATCAATCA 1560  
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 Db 1561 cagccatccGAGGCGCTGCGCAGAGCATATGAGAGGTGTCATCAGAGTTCGCAC 1620  
 QY 1621 AGAAGCTCACTCAAAAGGTGCTTCTTCAACACACGAGCCCTGAGAGACTCTGAAT 1680  
 Db 1621 agaagctcaCTCAAAAGGTGCTTCTTCAACACACGAGCCCTGAGAGACTCTGAAT 1680  
 QY 1681 CCTTCTCTACGCTCATGTATCTCGGTGGCGCAGCGGCTACTTACTCATGCTCGCTATG 1740  
 Db 1681 ccttctctTCTACGCTCATGTATCTCGGTGGCGCAGCGGCTACTTACTCATGCTCGCTATG 1740  
 QY 1741 CCTGTCTAACCAATGCTGCGCTGAGCTGCTCAAGTCCAGGGGCGCTGGGCTGGCTG 1800  
 Db 1741 cctgtctTAAACCAATGCTGCGCTGAGCTGCTCAAGTCCAGGGGCGCTGGGCTGGCTG 1800  
 QY 1801 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 Db 1801 ggtgctgctTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
 QY 1861 TTTCTTAAAGCTGCAACACTCAGTTTGGCATTTCTCGCTTGGTGGTGGTGGTGG 1920  
 Db 1861 ttctctTAAAGCTGCAACACTCAGTTTGGCATTTCTCGCTTGGTGGTGGTGGTGG 1920  
 QY 1921 ATGATGTTTTTCTTCTGCGCCAGCGCTTCAAGTGAAGACGAGAGTAAATGAATCCCT 1980  
 Db 1921 atgatgTTTTTCTTCTGCGCCAGCGCTTCAAGTGAAGACGAGAGTAAATGAATCCCT 1980









Db	2041	tcagaaatgtaacagccctcttcacatgagcggttaacccaattccgcctctgcggcgct	2100
Qy	2101	TCCTCCCTCCAGGACGAGGGTAGTAGTGCGTTCATATTTGGCATGGTTCTGCTCATTTTC	2160
Db	2101	tctccctccagagcagcgtagtagtgcgttcaattcttgcgaatgcttcgcattcttctc	2160
Qy	2161	CTGCAATTCCTCAGCATGGATTTTATATATCGACGCGGAGACACAGACATGGAAATTTTCGGCT	2220
Db	2161	ctgcacatctccagcatgattgattatatacgaacgcgaagacagagacatgattcttcgct	2220
Qy	2221	GTTTTACAAGCCCCCTGCGCTCACAGAGTATTCAGGTTCAACTCAAGGCTTACACGACGA	2280
Db	2221	gtttacaagagccccctgcgcacagagatgattcaggttgaactctgaagccttaacgcgaca	2280
Qy	2281	CACACGACAAATACCCGCTACAGCCCCCACCCTCCCTACAGACGACAGCTTTGCCATG	2340
Db	2281	cacacgacaaataccgcgtacagccccccaaactctccatacagcaqccaagattctgcacatg	2340
Qy	2341	AAACCCAGATTAACATGACAGTCCACTGTGTCCAGTCCCGACAGGAGTACGACCCCCACACGC	2400
Db	2341	aaaacgacagattaccacatgcagctccaaactctcagctccgacgaagatgcagacccccacacgc	2400
Qy	2401	ACGTGTACTACACACACCGGTGAGCCCGCTCCGAGATATCTGTGACAGCCGCTCACCGTGA	2460
Db	2401	acgtgtactacacacacccgcgttcgacgcgctccgaagatctctgtgcagcccgtaacgctga	2460
Qy	2461	CACAGAGACACCCCTACGCTCCACAGAGCCACAGAGACACACAGCTCCACAGGAGACCTGCTCT	2520
Db	2461	cacagagacacccctcagctcgcagagagccagagagcaccagctccacaaagagacctgtct	2520
Qy	2521	CCCAGTTTCCGACTCCAGCTCCACTGCTCGAGCCCCCTGTACGAAGTGCACACTCT	2580
Db	2521	cccagtttccgcactccagctccacactgcctcgaagccccctgtacgaagtggaacactct	2580
Qy	2581	CATCTTTTCTGGAAGCACTATGCTCCCTTCTTGAATCCAAAGCCCAAGAGTAGTGG	2640
Db	2581	catcttttctgcgaagcaactatgctccctctctcttgaaccaaaagccaaggtuagtgvg	2640
Qy	2641	TCATCTCTCTTTTCTGGGGCTTGCTGGGGTTCAGCCCTTATTTGGACACCACCAGTGAGAG	2700
Db	2641	tcatctctcttcttcttgcggcttgctggggttcgaagccttatabgcacaccagcagtgagag	2700
Qy	2701	ACGGCGTGGACCTTACGGACATTTGTACCTCGGAAACACAGAAATATGACTTTATTTGCTG	2760
Db	2701	agggactgcagccttaacgacatgtacctgcgcggaacacagaaataatgaccttattgctg	2760
Qy	2761	CACAAATCAAAATCTTTCTTTCTTACTAAACATGTATATATAGTACCCACCAAGACAGACTAC	2820
Db	2761	cacaattcaaaatccttcttcttcttaaaacaatgatatagtaaccacgaagaacgactaac	2820
Qy	2821	CGAATTTCCAGCACTTACTTTACGACTACACAGAGATTTCAGTAAAGTGAAGTATGTCA	2880
Db	2821	cgaataatccaagcaacttaactttaagacttaacaacggaggtttcagttaacgtgaagtatgtca	2880
Qy	2881	TGTTGGAGAAAAAACAACAGCTTCCCAAAATGTGGCTGCACCTACCTGAGAGACTGGCTTC	2940
Db	2881	tgttggaaagaaaaaacaaacagcttcccaaaatgtgcctgcactacttaagagactgccttc	2940
Qy	2941	ACGGACTTCAGATTTGATTTTGAAGTGAAGTGGGAAACCGGGAAATATATGCTCAAAACATTT	3000
Db	2941	aggaacttcaagatgtgatttgaagtgacgtcgggaacacgggaaaaataatgcacaaacatt	3000
Qy	3001	ACAAAGATGGATAGACAGATGAGTGCCTTCTCTACAAATCTCTGGTGCMAAACCGGACGC	3060
Db	3001	acaaagatggatagacagatgagatggaggtccttgcctatacaaaccttcctgcgtgcaaacgcgc	3060
Qy	3061	GGGATTAAGCCCATGCACATCAGCCAGTGTGAATAAACAGCTCTGTGTGATGACAGTGGCA	3120
Db	3061	gggataagcccatgcacatcagccagcttgacttaaacagctctcgtgtagatgcagatgcga	3120
Qy	3121	TCATTAATCCACAGCGTTTCTAATCTACTGTACAGGTTTGGGTGACGACGACCCCGTGC	3180
Db	3121	tcattaatccacagcgcttcttaatactcaacctgcgcgcttgcgtgtaagaacgacccgcgtgc	3180

QY	3181	CGAMGCGCCGCCAGGACATCCGCCACACCGGACCGAATGGGTCCACGACAAG	3240
Dp	3181	cgatgctgccccccagaccacaatccggccacaacggaccagaatggtgtccagacaag	3240
QY	3241	CCGACTACATGCGCTAAACAAAGGCTGAGATCCCGGACACAGGCCATCGACTATGCC	3300
Dp	3241	cggactacatgctgtaaaagaagctgagatacccggcagcagggcccatcgagtatgccc	3300
QY	3301	AGTTCCTTTTCTACTCAACGGGTTGCGGAGACCTCAGACTTTGTGGAGGCAATTGAA	3360
Dp	3301	agttcccttctacactcaacggtgtgcyggaacacctcagaactttgtgaggaatgaa	3360
QY	3361	AAGTAAGGACCTTCGACACTATACAGAGCCTGGGGGTGTCAGTTATCCCAACGGCT	3420
Dp	3361	aagtaagaacctctgcagcaactatacagaacctgcygggtgttccagttaccccaagct	3420
QY	3421	ACCCCTTCCTCTTGAGAGCAGTACATGGCCCTCGGCACCTGGCTGTGCTTCATCA	3480
Dp	3421	acctctctctcttcgagagcaatatactcgacctcgcaactgctgctgtctgtatca	3480
QY	3481	GGTGTGTGTGGCCCTGCATATTCCTGTGTGGCTGTCTTCCTTGTGAAACCCCTGGAGG	3540
Dp	3481	ggtgtgtgtgtggccctgcataatctctgtgtggcctgttcccttccctcgaacccctgagc	3540
QY	3541	CCGGGATCATTTGTGATGTGCTCGGCGCCTATGACGGTTCAGCTGTTCGGCATGAGGCC	3600
Dp	3541	ccgggatactatgtgatagtgtccctgagcgtgatagacgttcgagcttcgagatagtgcc	3600
QY	3601	TCATGGGAATCAAGCTCAGTGCCGCTGCCGTGTATCCTGTATCGCTTCTGTGGCATAG	3660
Dp	3601	tcatgggaatcaagctcaagtccagtgccgtgtgtctatcctcgaactcgtctctgtgacata	3660
QY	3661	GAGTGAAGTCAACCGTTCACGTTGTGGCCTTTCGAGAGGGCATGGCGGACAGAAAC	3720
Dp	3661	gagtgaagtcaacccgttcaacgttgccttgccttcttcgaagccatccgagcaagaacc	3720
QY	3721	GCAGGCGTGTGCTTGCCCTTGAGACATGTTTGACCCGCTTCGTGATGGCGCGTGTCA	3780
Dp	3721	gcaggcgctgtgtctgccccgagacatagtttgacccgcttcgtatgagcgctgtcca	3780
QY	3781	CTCTCTGTGGAGTGTGATGCTGTGGCGGAGATCTAGTTGCACTTATGTTCAGATATTCT	3840
Dp	3781	ctctctgtggagtgctgatagtcgtgcyggagatctgagttcgaacttcattgtcaagtaattct	3840
QY	3841	TTGTGTGTGTGGGATCTCACCATCTCGGCGTTCATGATGGGCTGGTTTGGTTCGCG	3900
Dp	3841	tgtgtgtgtgtgatactccacatactctcgsgtcttccaatgtgctgtttgtctccg	3900
QY	3901	TGCTTTTGTCTTTCTTTTGACCATATCTGAGGTGTCTCAGCCACGCGTTGACCGCC	3960
Dp	3901	tgccttgccttcttcttcttgacaatactcibaagtgltccagaaccaagcttgaaccgc	3960
QY	3961	TGCCCCACACCTCCCTTGAGGCCACCCGCCGCGGGTGCCTTGCCATGGCGCCGCGC	4020
Dp	3961	tgcctcaacacctctcccttgagccaccccccaagtggtgtgcgtctgcgcatagtccgcggcc	4020
QY	4021	ACACGCACAGCGGGTGTGATTCCTCGACTCGAGATTAAGTTCCACAGACGACAGTGTAG	4080
Dp	4021	acaagcacagcgggtgtgattctctccgaactcggagtaagtcccaagacgagatgtcac	4080
QY	4081	GGCTACGACGAGAGCTTGGGCATTCAGAGGCCACGAGGGCGGGGAGAGGCGCTGCCAC	4140
Dp	4081	ggtccagcagagagcttgcgacctacaagagcccaagcagcgcgcyggagggccctgcaccac	4140
QY	4141	AAGTATCTGTGAAGCCACAGAAAACCCGCTTCTTGCCCACTCCACTGTGGTCCATCCG	4200
Dp	4141	aagtatctgtgaaagcacagaataaccgcttctgcacaactccactgtgtctacatccg	4200
QY	4201	AATCCAGGATACACCACTCGAACCAGAGACAGACGCCCACTCGACTCAGGGTCCC	4260
Dp	4201	aatccaggatacaacacctctgaaccgcggaagacagaccacactggaactcaaggttccc	4260

OY	4261	TGCTTCCTCCGAGCGCAAGGCGCACAGCCCCGAGGGGACCCCCGAGGAAGGCTTGGTGGC	4320
Db	4261	tgcctccggaagcgcaagcgcaagcccccggaagcccccccaagaagagcttggcg	4320
OY	4321	CACCCCTTACAGACCGCGCAGAGAGCGCTTTTGAAATTTTCTAGGAAGGGCATCTTG6CC	4380
Db	4321	caaccctctacagacccgcgagagagcgtcttgaattcttactgaaaggcattctggcc	4380
OY	4381	CTAGCAATATAGGCCCCCTGGGGCCCTTGCGGGGGCCGTTCTCACAAACCCTGGAAACCAG	4440
Db	4381	ctagcaaatataggcccccttgggccccctgcggggccccgtcttcacaaacctgcgaaccag	4440
OY	4441	CGTCCACTGCATMGGGCAGCTCCGTGCGCGGCTACAGCCAGCCCATACACACTGTACGG	4500
Db	4441	cgctccactgcatamgggcagctccgtgcggcgctacagtcgccaagcccatcacacttgcagc	4500
OY	4501	CTTTTCGCTCCGTAAGTGTTCGCCGTGCACCGCGCGCTGTCCCTGGGCGTGGGGCGGAAC	4560
Db	4501	cttttcgctccgtaagtgcttcgcccgtgcacccgcgcgtgtccctgggctcgggcggaacc	4560
OY	4561	CCCGAAGGGGAGCTCTCCCAAGCTACCCGTAGACTGACACAGGCGCTGTGTGAGACCCCC	4620
Db	4561	cccgaaagggaactctgcacaggtacccgtagactgacacagcgccctgttggagaccccc	4620
OY	4621	ACGTGCGCTTCCACGTCGCGGTGTGAGAGGAGGATTCGAAAGTGGGAAGTGCATTAAGTGC	4680
Db	4621	acgtgccttccacgctcgcggctgtagaagagggatctcgaaggtagaagtcattgaagctgc	4680
OY	4681	AGGAGCTGGAAITCCGAGAGAGGCGCCGGGGAAGCACTCCAACTGAGGGCTGATTAAT	4740
Db	4681	aggagcttgaatctcgagagagggccccgggaagcagctccaactgagggctgattaaat	4740
OY	4741	CTGAAGCCAAGAGGCCAAAGATTGGAAACCCGCCACCCCACTCTTTCAGAACTGCGTT	4800
Db	4741	ctgaagccaagagggccaaagattggaaacccccccaccccccaacctcttccaagaactgct	4800
OY	4801	GAAAGAACTGGTTGGAGTTATGGAAGAAGTGCCTGTGCGAGACAGCAAGTTCAATGTT	4860
Db	4801	gaagaaactggttggagttatggaaagaagtgcctcggctgcgaagaaacgcgttcattgct	4860
OY	4861	ACTGTACCCGATGTGATTTATTTGTTAAATATTTCATTAATATTTTAAAGATGTACACA	4920
Db	4861	actgtaacccgatgtgattatttgttaaatatttctlaaataatttaagagctgtacaca	4920
OY	4921	TGCTGAATATACGAAGAGAGATGTAAAGTGTATGATCTGGGGCTTCTCACTCCTGCC	4980
Db	4921	tgtgtaaatatcgaagagagatgtaaagtgtaagtgtatgatactggggctctccactcctgc	4980
OY	4981	CCAGAGTGGGAGGCGACAGTGGGGGCTCCGCTATTTTGGCATTTGGGCGCGCTGCACA	5040
Db	4981	ccaagtgctggggcgacaacgctggggcccccgatctctgtgcacttggggccccgtgcaca	5040
OY	5041	ACCAAGCTTCATTAAGTCTTAAATTTCCAGCATATGTGTGCTGCTCTTAAATATGTATAT	5100
Db	5041	accaagcttcattagtccttaaatcttcagatagctgcgcgtccttaaatatgtataat	5100
OY	5101	TTACTTGTATATTTCTATGCAAATATTTGCTTATGTATATAGGATTAATTTGTAAAGCTTTC	5160
Db	5101	ttacttgtataattctatgcaaatattgcttatgtataagattatttgtaaagcttc	5160
OY	5161	TGTTTAAATATTTTAAATTTGCAATATCCACACCCTGTGGTAGTATGAATGTACTGTT	5220
Db	5161	tgtttaaaatattttaaatcttgcatacacaaacccgtgtgtatgtaaatgttactgtt	5220
OY	5221	AACTTTCAAACAGCGCTATGCGTGATAAATTTTGTGTATGAGCGAGATATGAAGAAGC	5280
Db	5221	aactttcaaacacgctatagcgtgtataatttcttgtttaatgagcagatatgaaagaagc	5280
OY	5281	CCGGAATTT 5288	
Db	5281	ccggaatt 5288	

RESULT	4	
ID	V15949	standard; cDNA: 6568 BP.
XX	V15949;	
XX	27-MAY-1998	(first entry)
XX		
DE		Nevoid basal cell carcinoma syndrome (NBCCS)(PTC) protein encoding cDNA.
XX		
KW		Nevoid basal cell carcinoma syndrome; NBCCS: PTC; PATCHED; detection;
XX		tumour suppressor; human; mutation; Gorlin's syndrome; ss.
OS		Homo sapiens.
Key		Location/Qualifiers
5'UTR		1..441
FT		/atag= a
FT		442..4332
FT		/atag= b
FT		/product= "NBCCS (PTC) protein"
3'UTR		4333
FT		/atag= C
XX		
PN	W09743414-A2.	
XX		
PD	20-NOV-1997.	
XX		
PF	16-MAY-1997;	97WO-US08433.
XX		
PR	16-MAY-1997;	97US-0017906.
PR	17-MAY-1996;	96US-0017906.
PR	21-MAY-1996;	96AU-0000011.
PR	07-JUN-1996;	96AU-0000363.
PR	14-JUN-1996;	96US-0019765.
XX		
PA	(USSH ) US SEC DEPT HEALTH.	
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.	
XX		
PI	Childamaram A, Christiansen J, Dean MF, Gallani MR;	
PI	Gerrard B, Gillies S, Goldstein A, Hahn H, Holmberg E;	
PI	Leffell DJ, Negus K, Pressman C, Shanley S, Smith I;	
PI	Unden AB, Vorechovsky I, Walwright B, Wicking C;	
PI	Zaplatopoulou PG, Chevenix-Trench, Toftgard R;	
XX		
XX	WPI: 1998-008883/01.	
DR	P-PSDB; W47157.	
XX		
PT		Nevoid basal cell carcinoma syndrome tumour suppressor gene - useful
XX		for detection of predisposition to basal cell carcinoma(s)
XX		
XX	Claim 1; Fig 8; 148pp: English.	
XX		
CC	This cDNA encodes encodes a nevoid basal cell carcinoma syndrome (NBCCS)	
CC	(PTC) protein. This nucleic acid specifically hybridises, under stringent	
CC	conditions, to a second nucleic acid consisting of a 6568 (full-length	
CC	sequence), 1732 (exon 1a, b) (V15998) or 659 (exon 2a) (V15999) base pair	
CC	sequence, in the presence of a human genomic library. The PTC polypeptide	
CC	when presented as an antigen elicits the production of an antibody which	
CC	specifically binds to a polypeptide encoded by the above three sequences.	
CC	The NBCCS gene and its protein product, is a tumour suppressor, and is a	
CC	homologue of the Drosophila PATCHED (PTC) gene. Detection of the NBCCS	
CC	nucleic acid, in particular abnormal sequences, by hybridisation assays	
CC	is useful for detecting a predisposition to NBCCS or to a basal cell	
CC	carcinoma (also known as Gorlin syndrome). Alternatively, detection is of	
CC	the polypeptide and is carried out by immunassay. Vectors comprising	
CC	this nucleic acid can be used to treat NBCCS. The PTC polypeptide can	
CC	mitigate symptoms of NBCCS in an organism. The NBCCS nucleic acid	
CC	includes one or more mutations, chosen from Exon-5 693insC, Exon-17	
CC	2988del8bp, Exon-21 3538delG, Exon-22 64302T, Exon-12 1711insC, Exon-17	
CC	1639insA, Exon-16 2707delC, and Intron-17 3137-2A to G. The mutation may	
CC	be a nonsense or frameshift mutation. Frameshift mutations are chosen	
CC	from 244delCT, 27insA, 464insAC, 693insC, 804del137, 877delG, 929delC,	

CC 1370del176, 1393insTGCC, 1444del16, 1497dup8, 1639insA, 1711insC,  
CC 2183delATC, 2320insAA, 2392delA, 2574delA, 2585delC, 2596complex,  
CC 2707delC, 2740insC, 2749dup7, 2988del18bp, 3014insA, 3352delAT and  
CC 3538delG. The mutation may be missense, chosen from G391T, G118A,  
CC G1568A, G1525T, C2050T, C3015A, G3193C AND G4302T. Alternatively,  
CC the mutation alters mRNA splicing and is chosen from A1055-2C, 3157-2A to  
CC G and 1493-8ins21. All these mutations are claimed but their sequences  
CC are not provided in the specification.

XX Sequence 6568 BP; 1499 A; 1780 C; 1676 G; 1610 T; 3 other;

Query Match 88.6%; Score 4684.8; DB 19; Length 6568;  
Best Local Similarity 99.7%; P-Val. No. 0;  
Matches 4692; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 585 GGAAGAGCTACTGCGCGGAAGCGCCACTGCTGAGAGGAGGAGTTTACAGACTCTTA 644  
DB 190 gggaaagctactgcccggaaagcgcgcgtgctgagagaggaagttccaaagactctta 249  
QY 645 TTTAAACTGGTTGTTACATTTCAAAAAAAGTGGCAAGTTCTTGTTGTGGCCCTCTTC 704  
DB 250 tttaactggtgttactatcctcaaaaaactgcgcgaagttcttggttggtggtcctc 309  
QY 705 AATATTGGGGCTTCGCGCGTGGGATTTAAAGCAGCACTCGAGACCAAGTGGAGAG 764  
DB 310 aatttggtggtcctgcgcgtggtggtttaaagcagcaactcctgagaccacgttgagag 369  
QY 765 CTGTGGGTGGAAGTTGGAGAGCAGTAAAGTGAATTAATTAATTAATTAATTAATTA 824  
DB 370 cgtggtggtgaggttgagagagcagagtaagtcgtgtaataataatactcgcagagagtt 429  
QY 825 GGAGAAGAGCTATGTTTAAATCTCAATCATGATACAGACCCCTTAAGAAGAGTGTCT 884  
DB 430 ggaagaagagctatggtttaaactcctcaactcatgatacagacccttaagaagaagtgct 489  
QY 885 AATGTCCTACACACAGAGGCTCTCAACACCTGAGACTGGGACTCCAGCCGCGCT 944  
DB 490 aatgtcctgacacagagagctcctcaacacactgagactcgcagctcagccagccgt 549  
QY 945 GTTCATGTATACATGTACACAGCAGCAGTGAATTTGAACATTTGTGTACAAATCAGA 1004  
DB 550 gtccatgatactatgatacaacagagcagtgaaattggaaccttggtgtacaaatcagga 609  
QY 1005 GAGCTTATACAGAAACAGGTTACATGATCAGATTAATGAATATCTTTACCCCTTTGG 1064  
DB 610 gagctatcacagaacaagttacatgatacagataatataatcttacccttggttg 669  
QY 1065 ATTATATACCTTTTGACACTGCTCTGGGAAGGGGCAAAATTACAGTCTGGACAGCATAC 1124  
DB 670 attattacaccttgagactgctcttggaagggcgaattacagctcgggagacagcatac 729  
QY 1125 CTCTAGTAAACCTCTCTTGGCGGTGACAACTTGACCCCTTTGGAATTCCTGGAAGAG 1184  
DB 730 ctctcctagtaaacctcctcttggtggtgacaaacttcgaaccttcggaattccttgaaag 789  
QY 1185 TTTAAAGAAATTAATCTATCATGAGTGACAGCTGGGAGGAATGCTGAATTAAGCTTGAAGTT 1244  
DB 790 ttaagaanaataaatacatcaagtcgagcagctggaagaaatgctgaataagctgaagtt 849  
QY 1245 GGTCAATGTTTACATGAGACCGCCCTGCTCAATCCGCCGATTCAGATGCCCCGCCACA 1304  
DB 850 gtctatglttaacatgtagcgcctcctgctcaatccggtccggtccagatgccccgccaca 909  
QY 1305 GCCCCCAACAAAATTTCAACCAACCTTTGATATGACCCCTTGTGTTTGAATGATGATGT 1364  
DB 910 gcccccacaaaaatcacaacaaacctctgataatgaccttggtttgaaatggtgagtg 969  
QY 1365 CATGGCTTATCCAGAAAGTATATGACATGCGAGAGAGAGTTGATTTGGTGGACAGATC 1424  
DB 970 catgcttatccagaagaatataatgactgagcagagagtgatgttggtggtgacagctc 1029  
QY 1425 AAGAACAGACACTGGAAGAAACGCTGACAGGCCCATGCTCCGACAGACATGTTCCAGTTAATG 1484

DB 1030 aagaaacagcactggaataaactcgtcagcgccatcgtccctcagacactgttcagtaactg 1089  
QY 1485 ACTGCCAAGCAAAATGTACAGACACTTCAAGGGGTACAGATATGTCACACATCAACTCG 1544  
DB 1090 aactcccaagcaaatgtaagagcactcctcaaggggtacagatagttcacaacatacaactgg 1149  
QY 1545 AACGAGACAAAAGCGGACGACATCTCTGAGAGGCGCTGGCAGAGACATATGTGAGTGTGTT 1604  
DB 1150 aacgagacaagaacgagcagcatcctctgtaggctctgacagagacataatgtgaggtgtt 1209  
QY 1605 CATCAGAGTGTCCGACAGACAACTCCACTCAAAAAGTGTCTTCTTACACACAGACCTTG 1664  
DB 1210 catcaagtgctgcagacaagaactccactcaaaagtgtcttccctcccaacagacactg 1269  
QY 1665 GACGACATCCCTGAATATCTCTCTCTACAGCACTGATGATCATCGGCTGGCCAGCGCTCTTA 1724  
DB 1270 gaagacatcctgaaatcctctctcgtcagtgcaatccgcgtgagcagcggtactctta 1329  
QY 1725 CTCAATGCTGCGCTATGCTGTCTTAACCATGCTGCGCTGGAGACTGCTCAAGTCCAGGGT 1784  
DB 1330 ctcatgtctgcctatgctcgtcttaacacatgctgcgtggtgactgtcccaagttccaggt 1389  
QY 1785 GCGGTGGGGCTGCGTGGGCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1844  
DB 1390 gccgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1449  
QY 1845 TGCTCATTTGATCGGAATTTCTCTTAAAGCTGCAACACCTCAGATTTGCAATTTTCGCT 1904  
DB 1450 tgcctcatgctcagaaatcctccttcaagctcgaacaaacacaggtttgccaatctcgtc 1509  
QY 1905 CTGTGTTGTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1964  
DB 1510 ctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1569  
QY 1965 AATTAAGAAATCCTTTTGAGAGACAGACGCGGGAGTGGCTTAAGCGCACAGAGCAGC 2024  
DB 1570 aataaagaatcccttltgaagacagacgagcaggtgtgtgtgtgtgtgtgtgtgtgtgt 1629  
QY 2025 GTGCGCCCTACAGTCCATGAGCAATGTCACAGCCTTCTTATGAGCGCGTTAACTCCAAAT 2084  
DB 1630 gtgagcctcagctcagatcaagaatgtcagaagctccttcaatggtcggttcaatcccaat 1689  
QY 2085 CCGGCTCTGGGGGCTTCTCTCTCCCTCCAGGACGAGGAGTAGTGTGTTCAATTTGGCATG 2144  
DB 1690 cccgctctgcggtggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1749  
QY 2145 GTTGTGCTGATTTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTT 2204  
DB 1750 gtctgtcctatcttctcgtcaatctcagatgataatcagacagcagagagagga 1809  
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QY 2265 CAGGCTTACACGACACACAGACGACAAATACCGCTACAGCCGCCACCTCTCTACAGCAGC 2324  
DB 1870 caggtcttaacacgacacacacagcaataaccgctacagccccccacctcctcagcagc 1929  
QY 2325 CACAGCTTTGCTTGAAGACGAGTTTACATGCACTGCACTGCTGCACTGCTGCACTGCTG 2384  
DB 1930 caacagcttgcacatgaagaacagatltacacagctcagctcagctcagctcagcagag 1989  
QY 2385 TACGACCCCGACAGCAGCAGTGTATACACACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 2444  
DB 1990 taagaccccccaagcagcagtgatctacacacacgcgtgagcgcgtcgcagatctctgtg 2049  
QY 2445 CAGCCGTCACCGTGTACACAGAGACACCTCAGCTCCAGAGCCCAAGAGACACACACTCC 2504  
DB 2050 cagcccgctcaacgtagacacagacacccctcagctgcagagagccagagacacacagctcc 2109  
QY 2505 ACAAGGACCTGCTCTCCCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCTGCAATTTCT 2564

Db 2110 acaaggaaactgctctcccaagctctccgaactccacactgctccagccccctgt 2169  
QY 2565 ACGAAGTGGACACTCTCATCTTTTGGCTGAGAAGCACTATGCTCTTCTCTTGAACCA 2624  
Db 2170 aagaaagtgagaaactctacactctcttgctgagaaagcaactatgctctctcttgaaacca 2229  
QY 2625 AAAGCCAAAGTAGTGTGTGATCTTCTTTTCTGGGCTTGTGGGGTCAAGCCTTTATGSC 2684  
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QY 2685 ACCACCGGAGTGGAGAGAGGGGCTGAGCTTACGACATTTGTACCTCGGGAACCGAGAA 2744  
Db 2290 accaccgagtgagagagagggctggaactcagacattgtaccccggaacccagagaa 2349  
QY 2745 TATGACTTTATGTGTCACAAATTAATTAATTTCTTTCTACAGATGATATAGTACAC 2804  
Db 2350 tatgacttattgtctgacaaacttaactctctctctctctctctctctctctctctctct 2409  
QY 2805 CAGAAAGCAGACTACCGCAATATCCAGACATTAATTAATTAATTAATTAATTAATTAAT 2864  
Db 2410 cagaaagcagactaccgcaataccagcaacttaacttaacttaacttaacttaacttaact 2469  
QY 2865 AACGTGAAGTATGATTTGTGGAAGAAACAAACAGCTTCCCAATGTGGCTGACTAC 2924  
Db 2470 aagctgaaagtagtcaatgtctggaagaaacaaacagctctccaaatgtgagctgacac 2529  
QY 2925 TTCAAGACTGGCTTCAGAGGACTTCAGAGTGCATTTGACAGTGGGAAACCGGGA 2984  
Db 2530 ttcaagagactgcttccagggacttcaagatgcatcttgacagtgacttggaacccgggaaa 2589  
QY 2985 ATCATGCCAAACATTTACAAATGTGATCAGACGATGGAGTCTTGTCTTACAACTCTG 3044  
Db 2590 atcatgccaacaaatlaaanaalbgatcagaacgaatggatctctgcttcaacaaactcag 2649  
QY 3045 GTGAAACCGGCGAGCGGATGAAGCCCATCGACATCAGCAATTTGCTTAACAGGCTG 3104  
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QY 3225 TGGGTCCACGACGAAGCGGACATGCTGCTGAACAGGCTGAGATCCCGGACGAGAG 3284  
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QY 3285 CCCATCGATATGCGCAGTTCCTTTCTACCTCAACGGGTTGGGAGACCTCAGACTTT 3344  
Db 2890 cccatcgatatagcccagcttcccttctacacacacacacacacacacacacacacacac 2949  
QY 3345 GTGAGGCAATTTGAAAAGTAAGACATCTGACGCAACTATACAGCCTGGGCTGTCC 3404  
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QY 3405 AGTAAACCCCAAGGCTACCCCTTCTCTTGGGAGAGTACATGGGCTCCGCACTGG 3464  
Db 3010 agttaaaccacaagctaacccctctctctctctctctctctctctctctctctctctct 3069  
QY 3465 CTGCTGCTGTTCATCAGCGCTGTGTGGCTGACATTCCTGCTGTGGCTTCTCTCT 3524  
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QY 3525 CTGACCCCTTGACGCGCGGAGATCATTTGTATGCTGTGGGCTGATGACGCTGACGCTG 3584  
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QY 3585 TTGCGCATGATGGGCTCATGGAATCAAGCATGAGTGGCGGCTGGCTCATCTCATGATC 3644  
Db 3190 ttgcatgtatgggctcatcagacacacacacacacacacacacacacacacacacacac 3249

QY 3645 GCTTCTGTGATAGAGTGAATTCACGTTACGTTGCTTTGGCTTTCTGACGCGC 3704  
Db 3250 gcttctgtgcatagagtagaggttacacgcttaacgtgtgtgtgtgtgtgtgtgtgtgtgt 3309  
QY 3705 ATGCGGACAGAACCGCAGGCTGTGCTTGCCTTGAGACATGTTTGGACCCGCTCG 3764  
Db 3310 atcgagcaagaacccgagggctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3369  
QY 3765 GATGGCGCCGTGTCACATGCTGAGTGTGTGATGCTGGGAGATCGATTGAGCTTC 3824  
Db 3370 gatggcgccgtgtcactcctcgagagtgctgacatgcgagcgagatccgacttc 3429  
QY 3825 ATTGTACGATTAATTTGCTGTGCTGCGATTCCTCAACATCTCGGCTTCTCAATGG 3884  
Db 3430 atgtcagatattctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 3489  
QY 3885 CTGCTTTTGTCTCCGCTGCTTTTGTCTTGTGACCATATCTGAGTGTCTCAGCC 3944  
Db 3490 ctgtttgtctccgctgtcttcttctcttcttgacacatactctgagtgctccagcc 3549  
QY 3945 AACGCTTGAACCGGCTGCGCACACCGCTGAGCCACCCCGAGGCTGCTCGCTTC 4004  
Db 3550 aacgcttgaaacgctcgccacacacacacacacacacacacacacacacacacacacac 3609  
QY 4005 GCCATGCGCGCCGCGCACAGCGAGCGGCTGTGATTCCTTCCGACTGATATAGTTCC 4064  
Db 3610 gccatgcgcgccgcgccacacacacacacacacacacacacacacacacacacacacac 3669  
QY 4065 CACACGACATGTAGAGCTTCAGGAGAGCTTGGGCACTACGAGCGCCAGCGGCGG 4124  
Db 3670 cagacgacatgttagagcttccagagagagagcttgcagactcagagccagagcgcg 3729  
QY 4125 GAGAGCCCTGCCACCAAGATGATGTGGAAGCCACAGAAACCCGCTTGGCCACATCC 4184  
Db 3730 gagagccctgccacacacacacacacacacacacacacacacacacacacacacacac 3789  
QY 4185 ACTGTGCTCATCCGATCCAGATCCAGGATCACCCACCTTGAACCCGAGACAGCCCCAC 4244  
Db 3790 actgtgtcatctccgatactcaagcatcaacacacacacacacacacacacacacacac 3849  
QY 4245 CTGAGCTCAGAGGTTCCTGCTCCCGGAGCGCAAGGCCAGCGCCGAGGAGCCCGCC 4304  
Db 3850 ctgagctcagaggttccctgcttcccgagcgagagcagcccgagagagacccccc 3909  
QY 4305 AGAAGAGCTTGTGGGACACCCCTTACAGACCGGCGAGAGCGCTTGAATTTCTACT 4364  
Db 3910 agaagagcttgygcaacccctcacagacgagagagagcttctgaattctcactc 3969  
QY 4365 GAAGGGCATTTCTGGCTTACCAATAGGGCCGCTGCGGGCCCTCCGCGGCCCTTCTCAC 4424  
Db 3970 gaagggcatcttgcccttagcaatagggcccgctcgggccctcgcgggccctctctac 4029  
QY 4425 AACCTTCGGAACCCAGCTCCTGCTGCGGAGCTGCGGCTGCTGCTGCTGCTGCTGCTG 4484  
Db 4030 aaccttcggaacccaagctcactgagcagctcctgctgctgctgctgctgctgctgct 4089  
QY 4485 ATCACCAGTGAAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4544  
Db 4090 atcacacgtgagcggtctctctctctctctctctctctctctctctctctctctctct 4149  
QY 4545 GGGCTGGGGGGAACCCCGAGGGGAGCTGCGCCAGGCTACCTGAGACTGACACGCGC 4604  
Db 4150 gggcctggggggaaccccgagggagctctgcccagctacaccttgagactcagacaaagc 4209  
QY 4605 CTGTTTGTGAGACCCCACTGCTTCTTCAAGTCCGCTGCTGAGAGAGGATTCGAAGTG 4664  
Db 4210 ctgtttgtgagaccccaactgcttctcaagctcgggtgtgagagagagatcgaaagtgt 4269  
QY 4665 GAAGTATGAGTGGAGCGAGCGAGATGAGAGAGAGGCGCGGAGAGAGAGTCCACAC 4724  
Db 4270 gaagtaatgagctgagagagctggaatcgagagagagagagagagagagagagagagac 4329

Oy	4725	TGAGGGGTGATTAAATGTGAAGCAAAAGGGCCAAAGATTGGAAACCCCGCACACCT	4784
Db	4330	tgaggggtgattaaatctggaagcaaaaggccaaagatctggaaccccccacccact	4389
Oy	4785	CTTTCACGAACCTCTTGAGAGAACTGGTTGGAGTTATGAAAGAAGTGCCTGTGCAGG	4844
Db	4390	ctttccagaaactcttggaagaaactcgttgagtgatgagaaaagatgcctcgtgcagg	4449
Oy	4845	ACAGCAGTTTCATTGTTAAGTGAACCGATTGTATTATTTGTTAAATTTCTAATAATAT	4904
Db	4450	acagcagttatctgttactcgttaaccgattgtatattctgtttaaattctctaataat	4509
Oy	4905	TTAAGGAGTGTACACATGCTGTAATATATGGAAGGAAGGATGTAAGTGATGTCGGGG	4964
Db	4510	ttaaaggagatgtacacatgltglaatalaggaaagagatglaaagltglatgcttgggc	4569
Oy	4965	CTTCTCCACACCCCGCCCAAGTGTGGAGGCCACAGTGGGGCCTCGCTATTGTGAT	5024
Db	4570	ctttctccactccctcgccccagaagtgtggagggccacagctgggacctctgtatttggcat	4629
Oy	5025	TGGGCTCCGTCGACAAACCAAGCTTCATTAGCTTTAAATTTGAGATATGTGCTGTC	5084
Db	4630	tgggctccgycgccaacaaccaagcttcattagtcttaatttcagcatatgttcgctgc	4689
Oy	5085	TTAAATATTTGTTATTAATTTACTTGATATATCTGATGCAATATTCGTTATGTAATAGATT	5144
Db	4690	ttaaatattgtataatttacttgtataattctatgcaaatatgtcttactgtaataagatt	4749
Oy	5145	ATTTTGTAAAGGTTTCTGTTAAATATATTTAAATTTGCATATCAACCCGTGGTAGT	5204
Db	4750	attttgtaaaggcttctcgtttaaataattttaaatttcgatacaaacccgtggtagt	4809
Oy	5205	ATGAAATGTTACTGTTAACTTTCAAACAGCGTATGCGGATTAATTTTGTGTTAATGAG	5264
Db	4810	atgaaatgttactcgttaacttcaaacacgctatgcgtgtaataatttttgtttaatgag	4869
Oy	5265	CAGATATGAAGAAAGCCCGCAATT 5288	
Db	4870	caaatatgaagaagaagcacgtaatt 4893	
RESULT 5			
V21587			
ID	V21587	standard; DNA, 5187 BP.	
XX	AC	V21587;	
XX	DT	25-JUN-1998 (first entry)	
XX	DE	Precis coenia (butterfly) patched (ptc) protein encoding DNA.	
XX	KW	Patched protein; ptc; cancer; tumour suppressor; cell adhesion promoter.	
XX	XX	wound healing; ageing; Precis coenia; butterfly; ss.	
XX	OS	Precis coenia.	
XX	PN	WO9745541-A2.	
XX	PD	04-DEC-1997.	
XX	PF	02-JUN-1997; 97WO-US09553.	
XX	PR	31-MAY-1996; 96US-0656055.	
XX	PA	(REGC ) UNIV CALIFORNIA.	
XX	PA	(STRD ) UNIV LELAND STANFORD JUNIOR.	
XX	PI	Epstein E, Goodrich LV, Johnson RL, Oro A, Scott MP;	
XX	DR	WPI. 1998-032648/03.	
XX	PT	Patched protein other than Drosophila melanogaster patched protein -	
XX	PT	used for characterising the phenotype of a tumour	

XX Claim 2; Pages 49-51; 86pp; English.

XX

CC This DNA is stated to encode a Precis coenia patched (ptc) protein and

CC is identical to the mouse ptc cDNA. This can be used to construct an

CC expression cassette comprising an altered patch or hedgehog gene. The

CC expression cassette comprises a nucleic acid encoding a patched protein

CC other than a Drosophila melanogaster patched protein, or fragment of at

CC least 12 nucleotides in length, as other than an intact chromosome under

CC transcriptional control of a transcriptional initiation region, and a

CC transcriptional termination region, both functional in an expression

CC host. A genetically engineered mammalian cell comprising this expression

CC cassette as an extrachromosomal element or integrated into the genome of

CC the cell can be predisposed to develop basal cell carcinoma as a result

CC of the transfection. By analysing DNA, functional analysts of patched

CC protein function, or by detecting antibody binding to abnormal patched

CC protein, a genetic predisposition to developmental abnormalities and

CC cancer can be diagnosed. This analysis can also be used for

CC characterising the phenotype of a tumour, particularly a carcinoma,

CC especially a basal cell carcinoma. The methods can also be used for

CC characterising transitional cell carcinoma of the bladder, meningiomas

CC medulloblastomas, etc. The modified cells comprising the expression

CC cassette can be used to determine the role of different exons of the

CC patched gene in oncogenesis, signal transduction, etc. Transgenic animal

CC models created from these cells can be used as animal models for

CC carcinomas of the skin. The patched protein of mosquito, butterfly or

CC beetle or alternatively, a mammalian patched protein of human or mouse

CC can be used to identify ligands or substrates that bind to, modulate, or

CC mimic the action of patched gene. These agents could be used as tumour

CC suppressors, cell adhesion promoters (e.g. in wound healing and ageing).

XX

XX Sequence 5187 BP; 1165 A; 1412 C; 1337 G; 1270 T; 3 other;

Query Match	71.9%:	Score 3801.2:	DB 19:	Length 5187:
Best Local Similarity	88.1%:	Pred. No. 0:		
Matches 4276:	Conservative 1%:	Mismatches 3:	Indels 516:	Gaps 11:
QY 446	CGGTGCCCCGGGACGGCCGCTGGAGGGCGGAGGGCGACAGAGCGGGGGGCTCGCGG	505		
Db 120	cggggcccttggcagagcaagcccgcggggagagccagagacggagccgggacccgaccg	179		
QY 506	TGCTGCGCGCCGGACCGGAGCTATCTGCACCCGGCCACGCTACTGCGAGCGCCGCTTGGC	565		
Db 180	c---gcgcgcgcgagccggagactatctgacgcgcgcagctactctgagagccgccttcgc	236		
QY 566	TCTGGAGCAGATTTTCCAGGGGGGAGGCGATACGCGCGGAAAGCCACACTGTGGCTACAGC	625		
Db 237	tcttggagacagatcttccaaagggaagcgctacatgcccgaagaagcgccgccttggctgagagc	296		
QY 626	GAGGTTTCAGAGACTCTTATTTAAACTGGGTGTATACATTCATAAAAAACTGGCGGACAT	685		
Db 297	gaagtttcagagactcttatttlaaaccttgggtgtgttactatccaaagaacatcgcggaagtt	356		
QY 686	CTTGTTGTGGGCTCTCTCATATTTGGSGGCTTGGCGGTGGGATTTAAAAACAGCAACCT	745		
Db 357	tttggtttgggtctccctccatatttggggcccttcgttggattaaagcagctaatct	416		
QY 746	CGAGCCCAACGCTGGAGGAGGCTGTGGGTGGAGTTGAGGAGCAGATGAATCGTGAAATTAA	805		
Db 417	cgaagcaacaagltggagagagcttgggtgggaagtttggtagcagtgagttcggaaattaa	476		
QY 806	TTTATCTGCGCAGAAGATTGGAGAGAGGCTATGTTTATCCTCAACATCATATTCACAGC	865		
Db 477	ttataccggtcagaagataggaagaagagctatgttlatctctcaaccatgatatacagac	536		
QY 866	CCCTTAAGAGAAGGTGCTTAATGTCTCTGACACACAGAGCGCTCTTAACAACACTTGAGCT	925		
Db 537	tccaaaagaagaagcgctaatgttctgacacacagaagctcttcctgcaaacacttgactc	596		
QY 926	GGCACTCCAGGCCAGCGCTGTCCATGTATACATGTACAAACAGCAGTGGAAATTGGACAC	985		
Db 597	agcactccagagcagctcgttgcacgctcattacatgatatacagagcagatggaaattgagaca	656		

[illegible]

QY	2066	GGCCGCGTTAAATCCCAATTCCCGCTTCGCGGGGTTCTCCCTCCAGGACACGCGTAGTACT	21235
Db	1737	ggccgatttgatccctccatccctccgcccctgcaagcgcttcctccccaagcgctgcgtggtgtg	17966
QY	2126	GGGTGTTCATTATTGGCATGGTTCGTGTCATTATTTCGTCGAATTCTCCAGTGGATTTATA	21855
Db	1797	ggatccaatttctgcatgattctgtctcatctttctctgcaattctcagaattgtcttata	18566
QY	2186	TCGACGCGAGGACAGGAGACTGGATATTTTCTGCTGTTTACAAAGCCCTCGCGTACAG	2245
Db	1857	caagcgtgagagacaagaagtctgataattctctgctgttccaaagcccctgtgcagcag	1916
QY	2246	AGTGATTACAGGTGGAACCTTCAGGCTTCACCCGACACACAGCAATATCCGCTACAGCC	2305
Db	1917	ggltgattcaagtltgagcccaagcgcttacaagagccttcaagtaatacaacccgttacaagcc	1976
QY	2306	CCCACTCCCTTCAGGACGACACGCGCTTGGCCATGAAAGCCAGTTACATGACGTCCAC	2365
Db	1977	cccaaccccatlacaacagccaaagcgtctgcgccaagaaaccaatactatctgtacgtcac	2036
QY	2366	TGTCCAGCTCCGACAGGAGTATACACCCCGACAGCATGTACTATACACACGCGTGAAC	2425
Db	2037	cgltgaagctccgcagaagagtatgacctcaacagaagtgtaactaaaccaacgcgcagacc	2096
QY	2426	GGGCTCCGAGATCTCTGTGACAGCCGCTCACCGTGGACACAGACACCTTCAGTCCAGAC	2485
Db	2097	agcgtctgagatctctgttacaagcgtlttaacgtccaccagaagaaaccttcaagctgttcaag	2156
QY	2486	CCGAGAGACACAGCTCCACAAAGGAGACGCTCCGCAATTCGCGATCCAGGCTCCGA	2545
Db	2157	tcccgagagacaacaagcttcaacagggaaacctccccaattcttcagaacctcaagcccca	2216
QY	2546	CTGCGTCGAGCCCCCTGTACGAAAGTGAGCACTCTCATCTTTTGTGAGAGAAGACTATGC	2605
Db	2217	ctgctctcgagcccccttgcacaagtgagaaactctctgttgcagaagaagactatgct	2276
QY	2606	TGCTTTCCCTCTTGAACCCAAAGCCAAAGTAGTGATGATCTTCTTTTGTGGGCTTGCT	2665
Db	2277	tcccttccctccctgaaaccccaaaagccaaagtlgtgtgtaatccttcttcttcgtggtctgtct	2336
QY	2666	GGGGGTCAACCTTTATGAGCACCCGAGTAGGAGAGAGGGCTCGACTTCGGGCAATGTT	2725
Db	2337	gggggtcagccttattatggaaccccccgaagtgaagaagggcgtggaacctcaagacattgt	2396
QY	2726	ACCTGGGGAACACAGAAATATGACTTTATTTGGTGCACAATTCMAATCTTTCTTCTA	2785
Db	2397	tcccgggaacacagagaatattgacttcaagcttcaagcttcaagtaacttcccttcta	2456
QY	2786	CACACATGTTATATAGTACCCGAGAAAGCAGACTACCCGAATATCCAGACTTTACTTTAGA	2845
Db	2457	caacaatglatatagttaccacagaagacagacttccgaatataccaagaccttacttacya	2516
QY	2846	CCTACACAGGACTTCAGTAAGCTGTAAGTATGTGATGTTGGAGAAACAAACAGCTTCC	2905
Db	2517	ccctcataagagcttccaagaatgtgaaagtatgtcatttgcgttgcgttgcgttgcgttgcgttgc	2576
QY	2906	CAAAATGTGGCTGCACTACTTTCAGAACTAGGCTTCAGAGGACTTCAGAGTTCATTGTACAG	2965
Db	2577	ccaattgtgcctgaactactttagaagactgcgtctcaagtaacttcaggaatgactttagcag	2636
QY	2966	TGACTGGGAACCGGGAATACTATGCCAAACAAATTACAGCAATGATCAGACGATGGAGT	3025
Db	2637	tgactggaagaaactggaagatcatgccaacaaatltlaaaatgtgatlagaatgaagggct	2696
QY	3026	CCTTGCCTAACAACTCTGTGGTGCAAAACCGGCACCGCCGATTAACCCATGCACATCAGCCA	3085
Db	2697	ccctgccttacaacactccctgtgtcgaagctgtgcagccgaagaacccatcgacatgtatca	2756
QY	3086	TTTTGATTAACAGCGCTGTGGTGGATGCACATGGCATCATTAATATCCAGCGCTTTCTCAT	3145
Db	2757	gttgacttaaacagcgctctgtgtagaagcagaatgtgacatcaatctcgaagcgcttcttcaat	2816
QY	3146	CTTACCTGACGCGTGTGGGTACGACACAGCCCGTCCGCTATGCTGCTCCAGGCGCAACAT	3205









QY	3806	GGGATCTGACGTTGACGTCCTCAATGTGCAGGATTTCTTTCGTCGTCGGGATCTCCATCAT	3865
Db	3477	agggtccgaattcgtattcattcattcagaatactctcttgcgctcctgacattccatcagct	3536
QY	3866	CCCTGGGCGTTCCTAATGGCGGTGTCTTTCGTCCTCCGTCCTTTTGCTTCTTTGGACCTTA	3925
Db	3537	ctctgggggtcttccataatgagactgtctctgcctgcctctctctatctctctcttgagcgtg	3596
QY	3926	TCCGTGAGGTCCTCCAGGCCAAGCGCTTGAAACCGCTCTGCCACACACCTCCCTGAGCCAC	3985
Db	3597	tccctgggggtgctcccgagcccaatgagcctcaaacgcagctgccactctctgcctgagccgc	3656
QY	3986	CCCCACGTCGTGTCGCGCTTCGCCATGCGCCCGCCGCGCACACGACAGCGGGTGTGATTCCTC	4045
Db	3657	tccaaagtgcgtccgtcttgcgtgcgtccctctctggtccaaagaacaaatgggtctgtattcttc	3716
QY	4046	CGACCTGGGAGCTATAGTTTCCAGACGACAGTCAGGCTCAGCGGCTCAGCGAGGACTTTCCGCACTA	4105
Db	3717	cgactctggagttacagctctctagaaccacggtgtctgtgcataagtgagagatctcagcaata	3767
QY	4106	CGAGCGCCACGACGAGCGCGCGGAGAGCCCTGCGCCACCAAGTATGCTGGAAAGCCACAGAAAA	4165
Db	3777	cgaaagacagcaggggtgcgcggagggccctgcgcccaaggtatgtgtgaaagccacaagaaa	3836
QY	4166	CCCCGTCCTTCCGCCACTCCACTGTGTGCATCCCGAATCCAGCGCATCCACCCCTGGAA	4225
Db	3837	ccctgctcttgcgcggcttccactgtgtgttccatcccgactccaagatcaagctctctctgac	3896
QY	4226	CCCGAATACGACAGCCCGCCACTCGTACGTCAGGGTCCGTCCTCCCGGAGCGGACGAAGCCACGA	4285
Db	3897	ccctcgcaaacagccccaactgtgactctgtctcttgcctctgcctgcgagcgcaaggtccagca	3956
QY	4286	GCCCGCCAGGAGACCCCCCAAGAGAGGCTTGTGCGCACCCCTCTACAGACCGCGCAGAGA	4345
Db	3957	gcttcctgaagagatctcccctctagaaaggtctgtgcgcaccccccttacaagacgycgcagaga	4016
QY	4346	CGCTTTTGAAATTTCTACGTAAGAGGAGATTCGTGACCCCTAGCAATAGCGCCGCGTCGGGCC	4405
Db	4017	cgcttcttgaaattctctactgaaagggatctctgcgcctgaagaatagagacgcgtctcaaggcc	4076
QY	4406	TTCGCGGGCCCGTTCTTCACAAACCTTCGGAACCCAGCCTCCACTGCATGTGCGAGCTTCGT	4465
Db	4077	ccgtgtgggcgcgttctccacaacccctgcgaacccaacgctccacgcgcatgggcagctctgt	4136
QY	4466	GCCCGGCTCTGCGAGCCCATCAACCACTGTGANGGCTTCTGCCTCGCTGACTGTCCGCGT	4525
Db	4137	gcccagctacatctgcagcccatccataccactgtgaggtctctgcctctggttgactgtctgt	4196
QY	4526	GCACCCGCGCGCTGTTCCTCTGGGCGCTGGGCGGAACCCCGAGGCGGAGCTGCGCCAG----	4581
Db	4197	gattcccccg-----ccttgagccctggggcgcaaccccccgaggggccctgtccaggtcta	4250
QY	4582	-----GCTAACCTGAGACTGACACCGGCGCTGTTTGAGGACCCCGACGTGCCCTTTCCACGT	4636
Db	4251	tgaagagctacactgtgagctgactacacggtgtattgttgagatctcccaatgctccttccaagt	4310
QY	4637	CCGGGTGAGAGAGGAGGATTCCAAAGGTGAGATTCATTGTGAGCTGCACAGAGTGGGAATGGCA	4696
Db	4311	caggtgtgagagagagagactcaaaaggtgaggtctcatagagctctacaggaacgttgaaagtgta	4370
QY	4697	GGAGAGGCCCGCGGAGACAGCTCCAACTGAGGGGTGATTTAAATCTGAAGCAAAAGAGGCC	4756
Db	4371	ggagagggcctgtggggagcagcttccaactgaaggttaattaaatctgaagcaaaaggcc	4430
QY	4757	AAAGATTTGGAACCCCCACCCCGCCACCTCTTTCCAGAACTGCTTGAAGGAACTGGTGTGG	4816
Db	4431	aaagatctgaaa-gccccgcgcccccaccccttccggaactgtctgaagagaaactgctgtg	4489
QY	4817	AGTTATGGAAAAAGATGCCCTGTGCGCAGGACAGCACTTCTATTGTACTGTAAACGATTTGA	4876
Db	4490	aattatg-----ggaaagcgatctcatgtgttactctgtaactgattgtta	4530

QY	4877	TATATTGTAAATATATTTCGATAAATTTAAAGAGATGTACACATGTTGTAATATAGCAAG	49356
		::	
Db	4531	ttatctkgygaataattctataataatttaaraagtgtaaca--tgtaatacatalg	45888
QY	4937	GAAGATGTAAAGTGTATGATGTGGGGCTTCCACATCTCGCCCGAGATGTGAGGCC	49966
Db	4589	aaatgtgtacaagt-ctatttctctgggctctccacactctgcccagaatlggggaacc	46477
QY	4997	ACAGTGGGGCTCTCCGTAATTTGTGATTTGGGCTCCGTCCGACACACCAAGCTTCAATAGT	50566
Db	4648	aca--ggggcccttcccctgtgtacatlgctctctgtgcacaacaaccaagcttaacttag	47055
QY	5057	CTTAAA-----TTTCAGCATATGTCGTGCTGCTTAATATTTGTAATTTACTTGT	51088
Db	4706	ttttaaaaaaatctccacagacatalgctgcgtctgcttaataatgtataattacttgt	47655
QY	5109	ATAATTTCTATGCMAATATTTAGCTTATGTAATAGATTATTTTGAAGAGTTTCTGTTAAA	51688
Db	4766	ataattctatgtaaatatgtctatgtataatagatta-cttgtaaaaggtcttcggttaaa	48244
QY	5169	ATATTTTAAATTTGCATATCACACCCTGTGTAATGTAAGTAATGTACTGTAACTTTCA	52288
Db	4835	atatcttaaatctgcatatcacacaacctgtgtagaatgtaattgttaacttg	48844
QY	5229	AACAGCATAGGTGATATTTTTTTTGTTAATGACACAGATATGAGAAAGC	5280
Db	4885	aacacgcatacggtgtgta-----ttgtttacagacacagacatagaagaanaac	49311

RESULT	7
V64099	
ID	V64099 standard; DNA; 5187 BP

AC V64099;

DT 26-JAN-1999 (first entry)

**Precis coenia patched gene**

Patched gene; ptc; diagnosis; treatment; developmental disorder;

KW sperm production; gene therapy; ss.  
 XY

05 Precis coenia  
yy

US5837538-A  
PN  
YY

PD 17-NOV-1998  
xy

PF 06-OCT-1995; 95US-0540406  
 XY

PR	06-OCT-1995;	95US-0540406
PR	07-OCT-1994;	94US-03107AF

XX  
XX  
(STPBD ) INTV LET AND CEMANEODS TINTOR  
PA

Goodrich TV Tobacco PI Coast ME  
XX

XX  
DB WPT: 1999-033461 /03

Nucleic acid encoding

transferrin - used to express poly:peptide(s), useful for diagnosis and treatment of developmental disorders

# healing of injured tissue

Example; column 21-26; 38pp; English

The present invention describes vertebrate and invertebrate patched (*ptc*) genes containing and encompassed by the nucleotide sequence of the

recombinant production of the protein. These in turn are useful: (1) for generating antibodies (Ab) and (2) for

Ligands (potential therapeutic agonists and antagonists). The *ptc* gene, or its fragments are used to isolate related sequences.









```
QY 686 CTTGGTTGGGCTCCTCATATTTGGGCTTCGCGGTGGATTAAAGCAGCGCACT 745
    |||||
Db 357 ttgggtgtgggtctctctcatatttggtgcttcgtgtggtatgaagcagtaattct 416
QY 746 CGAGACCAACGTGGAGAGCTGTGGGTGGAAGTTGAGAGCAGTAAGTCGTGAATTA 805
    |||||
Db 417 cgagaccaacgttggagaagctgtgggtggaagttggttggagcagtgagtcgaagatlaa 476
QY 806 TTATACCTCCGCAAGATTGGAGAGAGCTATGTTTAACTCCCACTCATGATACAGAC 865
    |||||
Db 477 ttataccgttcgaagaatcggagaagcgtacatglttaaccctcaactcgtatcacagac 536
QY 866 CCTTAAAGAGAAGGTGCTAATGTCTTGACACAGAGCGCTCTACAGACCTGTGACTC 925
    |||||
Db 537 tccaaagaagaagcgtcaatgttctgacacagagcgtctctctgtaaacacgtgagctc 596
QY 926 GGCACCTCCAGGCGCAGCGGTGCTCATGTATACATGTACACAGCAGTGGAAATTTGAGACA 985
    |||||
Db 597 agcactccagccagtcgtgtgacgtcttaacgtataaagaagcaatggaggttgaaca 656
QY 986 TTTGTTTCAAAATCAGAGAGCTTATCAAGAAACAGGTTACATGATGATTAATGA 1045
    |||||
Db 657 ttgtgtctcaaatcgaaggaacttcaagagacaggttacaatgatacagataataga 716
QY 1046 ATATCTTAACTCTGTTGATTATTAACACCTTTGACTGCTTCGGAGAGGCGGAAT 1105
    |||||
Db 717 ataccttaacctgtcttaactcaacttaaccttgacctgtcttggaaggggaaagct 776
QY 1106 ACAGTCTGGAGAGCATCTACTCTCTAGTAGTAACCTCCTTTCGGGTGGCAAACTTCGACC 1165
    |||||
Db 777 aaagtcgcggagacgtacactcctcagtgacctcttlaagtgagcaaaacttggacc 836
QY 1166 TTTGGAATTCGTGAAGAGTTAAAGAAATTAACATACTAAGTAGAGACAGTGGAGAAAT 1225
    |||||
Db 837 ctgggaattcccaagaaggtlaaagaataataactcaaggtgagacagcgggaaggaat 896
QY 1226 GCTGAATAAGGTGAGGTTGCTCATGTGTTACATGAGACGCGCCTGCTCAATCGGCGGA 1285
    |||||
Db 897 gctgaataaagcggaggttgcattggtacatgtagcagcgcttgcctcaaccagcgga 956
QY 1286 TCCAACTGCCCCGCGCACAGCCCCCAAAATTCACCAAAACCTTATATGAGCCCT 1345
    |||||
Db 957 cccgaatctgacctgacagacccctcaacaaatcaacaaaccccttgaatgtggccct 1016
QY 1346 TGTGTTGAATGGTGAATGTCATAGGCTTATCCAGAAATATATGCACTGGCAGAGAGAT 1405
    |||||
Db 1017 gtttctgaatgtgtgagttcaaggtttatccaggaagtatatgcatltggagaaggaagtc 1076
QY 1406 GATTGTGGGTGGCAGGTCACAAAGACAGCACTGGAACACTGTCAGCGCCCATGCTGCA 1465
    |||||
Db 1077 gattgtgggtgtgtacccgtcaagatgacactgtgaaactgttcaagcgtcaacgacctgca 1136
QY 1466 GACCATGTCAGTAAATGACTCCCAAGCAAAATGTACAGCACTTCAAGGGGTAGAGTA 1525
    |||||
Db 1137 aacctgttccagttatagactcccaagaaatgtatgaacacttcaaggggtcagactta 1196
QY 1526 TGTCTACACATCAACTGGAACGAGACAAAGCGCAGCCATCTTGAGAGGCTCGCCAGAG 1585
    |||||
Db 1197 tgtctctacaactcaactgtgaatgaaagagagcgagcgccatccctgtgagggccgtgagag 1256
QY 1586 GACATATGTGAGAGGTGTTCAATCAGATGTCCACAGAACTCCACCAAAAGGTGCTTTC 1645
    |||||
Db 1257 gaactaagtcggaggtgtgtcaacaagtgtgcccccaactcctcaactcaaaaggtgtctcc 1316
QY 1646 CTTGACACCAAGACCCCTGAGAGCATCTGAAATCCTTCTTGAGAGTGAAGTCAATCG 1705
    |||||
Db 1317 cttaacaacaacagaccctggagacatactcaaaatccctctctgtatgtatgtatccg 1376
QY 1706 CGTGCGCAGCGGCTACTACTCATGCTGCGCTATCTGTCATCAACCATGCTCGCGTGGGA 1765
    |||||
Db 1377 agtggccagcggtacactaagtgtctgtcctatgtcgttttaacatgtcgtcgctggga 1436
QY 1766 CTGCTCAAGATCCAGGAGCGCGTGGGCTGGGCTGGGCTGCTGCTGTTGCACTGTCAGT 1825
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Db 1437 ctgctcccaagctcccaagggtggcggtgggctggcgtggcgtctgtgtgtgtgctgtcagt 1496
QY 1826 GGCCTCAGAGACTGGGCTGTGTCATGTGATTCGGAATTTCTTTAAAGCTTCGACCACTCA 1885
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Db 1497 ggtctggagatctggccctctgtcctctgtatgttgccattcttttaagtgctggcaactca 1556
QY 1886 GGTGTTTGCAATTTCTGCTCTTGTGGTGGTGGTGGATGATGATGATGATGATGATGAT 1945
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Db 1557 ggttttgcggttctgtcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1616
QY 1946 CTTCAAGTAACAGAGCAAGTAATAAGATTCCTTTTGGAGCAGGACCGGGAGGTCCT 2005
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Db 1617 attcagtgaaacagagcaagaaataaagaagattccaatttggagaagagactgggaagtgct 1676
QY 2006 GAAGCGCAGAGAGCAGAGCTGGGCTGACGTCATCAACAGCAATGTACAGCCCTTCTTCAT 2065
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Db 1677 caagcgcaacggagcagcggtggccctcaactcaacagcaatgttcaaccgctctctcat 1736
QY 2066 GGCCTGCTTAAATCCCAATTTCCGCTCTGCGGCGCTTCTCCCTCAGCAGCGGTAGTACT 2125
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Db 1737 ggcgcgcatlgaacctatccctctgcccctggagcgttctccctccagagcgtgtgtgtgt 1796
QY 2126 GGTGTTCAATTTTGGCATGTTGCTGCTCATTTTCTCGCAATTTCTCAGATGATTA 2185
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Db 1797 ggtatcaattttgtgtatgtgttctgtcctatcttctctgcaattctcaagatgtatcata 1856
QY 2186 TCGACGCGCAGCAGAGCACTGGAATTTTCTGCTGTTTACAGCCCTGGCTCAGCAG 2245
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Db 1857 cagacgttgaagacagaagatltgatalatttctgtgttctcaacaagccctgtgtcagcag 1916
QY 2246 AGTGAATCAGGTTGACCTCGAGGCGCTTACACGACACACAGCAACATATCCGCTACAGCCC 2305
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QY 2366 TGTCCAGCTCCGCGACGGAGTACAGACCCCAACGCACTGTACTACACACCGCTGAGCC 2425
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QY 2846 CTTACACAGAGATTTCACTAAGCTGAAGTATGTCACTGTTGGAGAAAAACAAAGCTTCC 2905
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Db	2517	ccttcataaaggtttccagcaatgtgaatgtatgtatctgtcggggaggaacaagaactttcc	2576
Oy	2906	CAAAATGTGGCTGCACtACTTCTCAGAGACTGCGTTCAGGAGCTTCAGGATGcATTGTCAAC	2965
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Oy	2966	TGACGTGGGAACCCGGGAATAATCATCCCAAAACAATTACAGAAATGcATGTCAGACATGGAGT	3025
Db	2637	tgacctgggaanaactcgggaagatcatgcccacaacttaataaagtatccagatgacggggt	2696
Oy	3026	CTTGTCCCTCAAAACCTCCTGGTGCAAACCCGCGACCGCGATTAAGCCATCGACATCAGCCA	3085
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Oy	3086	GTTGACTAAACAGCGCTCTGTGTGGATGACAGATGGGcATCATTAAATCCACAGCGCTTTCTACAT	3145
Db	2757	gttgactaaacacggctctgtgtagaagcagatgycatcatcaataacgagcgtttctacac	2816
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Db	2817	ctactctgacgcgttggtgtcagaaagacccttgtagttactgctgccttccagggccaacat	2876
Oy	3206	CCGGCCACACGACACAGAAATGGGTCCACACAAAGCCGcATGATCGCTTGAACAAAGCT	3265
Db	2877	ccgycctcaacccgycggagtggtgtccatbacaagccagactacatbpcagagacgaagct	2936
Oy	3266	GAGATTCCCGGGAGCAGAGCCCATCGAGTATGCGCCAGTTCCTCTTACCTCAACGGGTT	3325
Db	2937	gagatctccagagcagcagagcccatcgtagtacgctcagttcccttctactctcaagycct	2996
Oy	3326	CGGGACACCTCAGACTTTGTGGAGGCAATTGAAAAATGAAGACCATCTGCAGCACTA	3385
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Oy	3386	TACGAGCCCTGGGGCTGTCCAGATTACCCCAAGGCGTACCCCTCTCTCTTGGGGAGCAGTA	3445
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Oy	3446	CATGGCGCTCCGCGACACTGTGCGTGTCTGTTCATCAGCGTGTGGCTGTGACATTCCT	3505
Db	3117	catcagcctcggccactgtcgtgtctatccatcagcgtgtgtcgtgcctgcgaacgtttct	3176
Oy	3506	CGTGTCCGCTGTCTTCTTCTGAACCCCTGAGACGCCGGGATATTGTGATGGTCCCTGGCC	3565
Db	3177	agtgctgcagcttctctctcttgaaaccccttggacggccggagatcatgtlcatgctccygc	3226
Oy	3566	GCATGATCAGCGTGCAGCTGTTCGGCAATGAGCGCCTCATGGAAATCAAGCTCATGCCGT	3625
Db	3237	tcgtatgacagcgtltgagctctcttgcgtatgagggcccatctggtatcaagctgagtgctgc	3286
Oy	3626	GCCCGTGTATCTCATCGCTTCTGTGGCATAGAGTGGAGTTCACCGTTCACGTTGC	3685
Db	3297	gcctcgtgcatcatccgtatgtcatctgttgcacatcgagtgagtgatctcacgltccacgtgc	3356
Oy	3686	TTTGTGCGCTTCTGACGGCCATCGGGCGACAGAACCGGAGGGCGTGGTGGCCCTGGAGCA	3745
Db	3357	tttgagccttcttgcagacccatcttggggagacaagaacacaaggcctatgctgcgtccygga	3416
Oy	3746	CATGTTTGACACCGCTCTGTGATGGCGCGCTGCACATCTCTCTGGAGTGCATGATCGGC	3805
Db	3417	catgttgcctcccgctctcgtgaagcggtcgtgtgtccactcgtcgttgggtgtactgtactgc	3476
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Oy	3866	CCGCGCGGCTTCTCAATGAGCGCTGTGTTTGTCTCCCGTCTTTTGTGTTTGTGAGCATA	3925
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Qy	4046	gcagctgcgagatgttattttccacagacacactgttcagggccttcacacgagacgtttccgacatga	4105
Db	3717	cgactccgtagtaacagctctccagaccaggtgtgtcgtcatcagtgtagagactcagcgaata	3776
Qy	4106	cgagccccaacagcggcgcgggagggcccttcccaacaaagtatcgttgaaagccnagaaaa	4165
Db	3777	cgaaacacacagcagcagggtgcgcgagagccctgcacacaaagtatgttggaaagcacaagaanaa	3836
Qy	4166	ccccctgttgcggccactccactcagctggtgtccatcccaaatccagagcatcaccacccctcgaaa	4225
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Qy	4226	cccgagacagcagccccactctgactcagaggtccctgcctcccgagcgcamaagccacga	4285
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Db	3957	gctctcgaaaggatccccctcagagaaggcttgcggccacccccctaacagacgcgcagaga	4016
Qy	4346	cccttttgaattttctactgaaaggagcattctggcccttagcamaatgagggccgctggggccc	4405
Db	4017	cgcttttgaatttctactgaaaggagcattctgcgtctagcaatagagacgcgtcagagcgc	4076
Qy	4406	ttccggggggccctgtttcacaaccccttgagaaacccagcgctcacnccatggcgagcgttcgt	4465
Db	4077	ccgttgaggccgcttctccaaacccctcggaaacccaaagctccacacgcgcaltggcagctctgt	4136
Qy	4466	ggccggcgctactgctcacaccatccatccactgtgagcggcttctgcctccgttgactccgcgt	4525
Db	4137	ggccagctactactgcagcccatcaacaaactgtgacggtctctgcgtctggtgtgtctgt	4196
Qy	4526	gcacccggccgctgttcccttggcccttgccgggaaccccccgaggggagcttgcgccag-----	4581
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Qy	4582	-----gcttaccctgagacgttaccacagcggcgttttgagagacccccacagctgcctttccacgt	4636
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Qy	4697	ggagagagccccggggaagcagctcccaactgaaggtgattttaattctgaacaaagagccc	4756
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Qy	4757	aaagattggaaacccccccacccccacccttcttcagaaactgcttgagagacagctgttgg	4816
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Db	4589	aaatgctgtacagt-ctatttctggggcctctccactctcgtccccagagtgggagagcc	4647
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Db	4648	acc--ggggcccttccccctgtgttaactgtgtcgttgcacaaaccaaacttaacttag	4705









PA (GETH ) GENENTECH INC.  
 XX De Sauvage FJ, Carpenter DA;  
 XX WPI, 1999-620428/53.  
 DR P-PSDB; Y43261.

XX New isolated human patched-2 gene, used to develop products for  
 PT treating, e.g. cancer and Alzheimer's disease -  
 XX Claim 1; Fig 1; 124pp; English.

XX This sequence encodes the human patched-2 (ptch-2) protein of the  
 CC invention. The patched-2 polypeptides are signalling molecules,  
 CC specifically for signalling and mediator molecules in the hedgehog (hh)  
 CC cascade which are involved in cell proliferation and differentiation.  
 CC They can be used for the treatment of disorders which are mediated at  
 CC least in part by hh, especially Dhh, e.g. testicular cancer. They can  
 CC also be used for treating degenerative disorders of the nervous system,  
 CC e.g. Parkinson's disease, memory deficits, Alzheimer's disease, Lou  
 CC Gehrig's disease, Huntington's disease, schizophrenia, stroke and drug  
 CC addiction. Patched-2 agonists can be used to treat gut diseases, bone  
 CC diseases, skin diseases, diseases of the testis (including infertility),  
 CC ulcers, lung diseases, diseases of the pancreas, diabetes, and  
 CC osteoporosis. Antagonists or agonists of patched-2 may be used for  
 CC treating disorders or creating a desirable physiological condition  
 CC effected by blocking hh signalling, especially Dhh signalling,  
 CC e.g. contraception or infertility treatment. The products can also be  
 CC used for detection, diagnosis, drug screening and production of  
 CC transgenic animals.

XX Sequence 4030 BP: 728 A; 1297 C; 1141 G; 864 T; 0 other;

Query Match 22.2%; Score 1176.4; DB 20; Length 4030;  
 Best Local Similarity 61.5%; Pred. No. 7.9e-245;  
 Matches 2058; Conservative 0; Mismatches 1221; Indels 69; Gaps 8;

591 GCTACTGCGGCGAAGCGCAGTGTGCTGAGAGCGAAGTTTCAGAGACTTTATTTAAA 650  
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 QY 711 GGGGCTTCGCGGTGGGATTTAAAGACGACCTCGAGCAACAGGAGGAGCTGGG 770  
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 Db 1862 ctgtctctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1921







RESULT 12  
 A09081  
 ID A09081 standard; CDNA; 3453 BP.  
 AC A09081;  
 XX  
 XX 10-AUG-2000 (first entry)  
 DE Human patched-like gene (PTCH2) coding sequence.  
 XX  
 XX Patched 2, PTCH2: tumour suppressor; familial melanoma CMM1;  
 KW familial adenomatous polyposis; hMOM; Michelin Tire Baby Syndrome;  
 KW sonic hedgehog; SHH; development; carcinogenesis; cytostatic;  
 KW basal cell carcinoma; gene therapy; chromosome 1p32-35; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 13..3453  
 FT /\*tag= a  
 PN MO200020037-A1.  
 XX 13-APR-2000.  
 XX 06-OCT-1999; 99WO-SE01784.  
 XX 06-OCT-1998; 98SE-0003393.  
 XX (KARO-) KAROLINSKA INNOVATIONS AB.  
 PA (PHAA) PHARMACIA & UPJOHN CO.  
 XX  
 PI Zaphiropoulos PG, Unden AB, Toftgard R, Rahnama F;  
 PI Hollingsworth RE;  
 XX  
 DR WPI: 2000-303645/26.  
 DR P-PSDB: Y92225.  
 XX  
 PT Isolated human protein capable of participating in human patched  
 PT gene/Sonic hedgehog pathway during embryonic development is used in  
 PT medication for treatment of condition involving tumors such as basal  
 PT cell carcinoma  
 XX  
 PS Claim 4; Page 45; 55pp; English.  
 XX  
 CC This cDNA is derived from the novel human patched 2 gene (PTCH2), which  
 CC has been localised by radiation hybrid mapping to chromosome 1p32-35  
 CC with DIS211 and W1404 as closest flanking markers and with an estimated  
 CC localisation 5.5 cR from DIS443. This region is often lost by LOH in  
 CC various different tumour types, such as neuroblastoma, melanoma and  
 CC breast and colon cancer. PTCH2 is a candidate gene for a tumour suppressor  
 CC gene in this region. It is also a candidate gene for involvement in  
 CC familial melanoma CMM1, modifier locus for familial adenomatous polyposis  
 CC hMOM1 and Michelin Tire Baby Syndrome. Splice variants of the PTCH2 gene  
 CC exist (see A09082-84). PTCH2 is capable of participating in the human  
 CC patched gene/Sonic hedgehog (PTCH/SHH) pathway during embryonic  
 CC development and/or carcinogenesis. The isolated human protein is useful  
 CC as a medicament for the treatment of a condition involving tumours such  
 CC as BCC (basal cell carcinoma). The nucleic acid is useful in gene  
 CC therapy, and for use as a probe, primer or a diagnostic agent.  
 XX  
 SQ Sequence 3453 BP; 600 A; 1135 C; 989 G; 729 T; 0 other;

Query Match 22.2%; Score 1171.6; DB 21; Length 3453;  
 Best Local Similarity 61.4%; Pred. No. 8,1e-244;  
 Matches 2055; Conservative 0; Mismatches 1224; Indels 69; Gaps 8;

QY 591 GCTACTGCGCGAAGCCGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAAA 650  
 DB 91 gctggagcccggaagcctcactctgcttctgctactcaggccctctcttct 150

QY 651 CTGGCTTGTACATTCAAAAAACTGCGCAAGTTCCTGTGTGGGCTCCCTCATATTT 710  
 DB 151 ctggagatgcg99atccagagacatctg9caagtgctctctcgg9acatctg9ccctt 210  
 QY 711 GGGGCTTCGCGGTGGATTAAGCAAGCAACCTCGAGACACACGCGAGAGCTGG 770  
 DB 211 ggggcccctggcatctagctccgcatcgcattatcgaacaactcggacaagctcgg 270  
 QY 771 GTGGAAGTTGAGAGAGAGTGAAGTCTGTAATTAATTAATCTGCGCAAGATTTGAGAA 830  
 DB 271 gtagaagtg99gagccgggtgagccagagctcagatctacacaaagagagctg99gag 330  
 QY 831 CAGGCTATGTTTAATCTCACTCATGATACACACCCCTTAAGAAAGAGTGTAAATGTC 890  
 DB 331 gaggtctgataaacctctagatcagatcagatacagaacgacgacgagag99gagaaacatc 390  
 QY 891 CTGACACAGAGAGCGCTCTACACACCTGAGCTCGACCTCCGAGCGAGCTGTCCAT 950  
 DB 391 ctcaacaccgaaagcaacttg9ctcccaacctcccaagccctcactcagtaaaagctcaa 450  
 QY 951 GTATACATGTACACAGGAGGTGGAATTTGGAACATTTGTGTACAATCAGAGAGCTT 1010  
 DB 451 gtatcactctatg99gagctcgtg9gattg9aacaacatcgtacaaagctcagagctcc 510  
 QY 1011 ATCAGAGAAGAGGTTTACATGATCAGATATATGAAATATCTTACCTCTGTTGATTT 1070  
 DB 511 ctatctgaaatg99gaaatgattgagcgaatgattg9aagctgttccgtcgtcgtcctc 570  
 QY 1071 ACACCTTTGAGCTGCTTGTGGAAGGGCGAATTTACGCTGGAGACAGCTTACCTCTTA 1130  
 DB 571 acccccctcgaactgtctctcgtg99gag99gagacaaactcgaag99gctccgactac 630  
 QY 1131 GGTAAACCTCTCTTGGGTGGAGCAAACTTGACCTTTGGAATTCGTGAAGTTAAAG 1190  
 DB 631 ggcgcgcgatalccagtg99gacaaacttgatccagagcagctg99gag99gctcgt 690  
 QY 1191 AAAATTAATATCAATGAGACAGCTGGAGAGAAATCTGTAATAGCTGAGCTGTGTCAT 1250  
 DB 691 ccccttgctccctctg99g99gctc99gag--ctgctagacag99gacaa99g99cag 747  
 QY 1251 GGTTCATGAGACCGCCCTGCTCAATCCGCGCAGCTCAGCTCCCGCCAGACGCCCC 1310  
 DB 748 gctcagctg99g99g99g99g99g99g99g99g99g99g99g99g99g99g99g99g 807  
 QY 1311 AACAAAATTCACCAAACTCTGTATATGAGCCCTGTTGAATGGTGTATGTCATGCG 1370  
 DB 808 aacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 867  
 QY 1371 TTATCCAGAAAGTATATGCACTGCGCAGAGAGAGTGTATTTGGGTGCGACACTCAAGAAC 1430  
 DB 868 ttctcccaaaatctcagctcagctcagctcagctcagctcagctcagctcagctcagctcag 927  
 QY 1431 AGCACTGGAAGAACTCTGACAGCGCCATCGCCCTGAGACAGCATGTTCCAGATTATGATGCC 1490  
 DB 928 ccccaag99gagctgctg99g99g99g99g99g99g99g99g99g99g99g99g99g99 987  
 QY 1491 AAGCAAAATTCAGAGACACTTCAAGGGTACGAGATATGTTCTCACATCACTGGAAGCAG 1550  
 DB 988 cgcagcctgacagagatctcgcg99gtgactatcagacaatgacatctgctg99gtgag 1047  
 QY 1551 GACAAAGCGGACGACATCTCTGAGAGCCTGCGACAGGACATATGTGTGAGAGGTGTTATCAG 1610  
 DB 1048 gagcag99cagcagcagctcagcagcagcagcagcagcagcagcagcagcagcagcag 1107  
 QY 1611 AGTGTGACAGAACTCCATCAAAAGGTGTTCTTACACACACAGCCTTGAGACAGC 1670  
 DB 1108 gcccctcgtgagagcctcccaagcagatcagctcctccccaacacccctgagatgac 1167  
 QY 1671 ATCTGAAATCTCTCTGACGTCAGTGTATCCGCTGGCCAGCGCTACTTACTCATG 1730  
 DB 1168 atctcgtcagctgtctctcgtgagctcagctcagctcagctcagctcagctcagctcag 1227  
 QY 1731 CTGCGCTATGCTGTATCAATGCTGCGCTGGAGCTGCTCAAGTCCCAAGGTCGCGTG 1790





RESULT 13  
 Z31729  
 ID 231729 standard; DNA: 2082 BP.  
 XX  
 231729;  
 19-JAN-2000 (first entry)  
 DE Human patched-2 coding sequence partial clone 16.1.  
 XX  
 DE Patched-2; ptcn-2; human; signalling molecule; hedgehog cascade; stroke;  
 KW cell proliferation; cell differentiation; testicular cancer; gut disease;  
 KW degenerative disorder; nervous system disorder; Parkinson's disease;  
 KW memory deficit; Alzheimer's disease; Lou Gehrig's disease; schizophrenia;  
 KW Huntington's disease; drug addiction; bone disease; skin disease; ulcer;  
 KW infertility; lung disease; pancreatic disorder; diabetes; osteoporosis;  
 KW therapy; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN M09953058-A1.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 02-APR-1999; 99WO-US07417.  
 XX  
 PR 15-APR-1998; 98US-0060939.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI De Sauvage FJ, Carpenter DA;  
 DR WPI: 1999-620428/53.  
 XX  
 PT New isolated human patched-2 gene, used to develop products for  
 treating, e.g. cancer and Alzheimer's disease  
 XX  
 PS Example 1; Page 96-97; 124pp; English.  
 XX  
 CC This sequence is a partial clone of DNA encoding the human patched-2  
 CC (ptcn-2) protein of the invention. The patched-2 polypeptides are  
 CC signalling molecules, specifically for signalling and mediator molecules  
 CC in the hedgehog (hh) cascade which are involved in cell proliferation and  
 CC differentiation. They can be used for the treatment of disorders which  
 CC are mediated at least in part by hh, especially Dhh, e.g. testicular  
 CC cancer. They can also be used for treating degenerative disorders of the  
 CC nervous system, e.g. Parkinson's disease, memory deficits, Alzheimer's  
 CC disease, Lou Gehrig's disease, Huntington's disease, schizophrenia,  
 CC stroke and drug addiction. Patched-2 agonists can be used to treat gut  
 CC diseases, bone diseases, skin diseases, diseases of the testis (including  
 CC infertility), ulcers, lung diseases, diseases of the pancreas, diabetes,  
 CC and osteoporosis. Antagonists or agonists of patched-2 may be used for  
 CC treating disorders or creating a desirable physiological condition  
 CC effected by blocking hh signalling, especially Dhh signalling,  
 CC e.g. contraception or infertility treatment. The products can also be  
 CC used for detection, diagnosis, drug screening and production of  
 CC transgenic animals.  
 CC  
 SO Sequence 2082 BP; 380 A; 672 C; 596 G; 434 T; 0 other;

Query Match 11.2%; Score 593.8; DB 20; Length 2082;  
 Best Local Similarity 62.7%; Pred. No. 4.9e-119;  
 Matches 960; Conservative 0; Mismatches 562; Indels 9; Gaps 2;

Db 146 ctggagatcgggatccagagacatgtgcaaaagtctctctctgagatgtgacctt 205  
 QY 711 GGGGCTTCGCGGTGGGATTAAAGCAGCAACCTCGAGCAACAGTGGAGCGCTGGG 770  
 Db 206 ggggcccctggcatlaagctcccgcatatgacataatgagaaacttggacaagctctg 265  
 QY 771 GTGGAAGTTGGAGCAGAGTAACTAGTCTGTAATTAATTAATTAATTAATTAATTA 830  
 Db 266 gtagaagtgagcagccgagtgagccagagctgtacatlaacacagagagagctgggag 325  
 QY 831 GAGGCTATTTTATCTCAACATCATATATACAGACCCCTAAAGAAAGAGTGTATATC 890  
 Db 326 gaggctgatacaccctctcagatgctatagacacgcgcagagagagagaaaca 385  
 QY 891 CTGACCAAGAAAGCGCTCTTACAAACACCTGAGCTGAGCTGAGCTGAGCTGAGCT 950  
 Db 386 ctcaaccgccgaagcaacttggcctccacatccagagcagccctcactgcaagataatcaa 445  
 QY 951 GTATACATGTACAAACAGGAGAGTGAATTTGTAATTAATTAATTAATTAATTAATTA 1010  
 Db 446 gtacactataggaagctcctgagatltgacaacatctgctacaagtcagagctcc 505  
 QY 1011 ATCAGCAAGAAACAGTATAGATAGATATATATATATCTTTACCTTTGATATTT 1070  
 Db 506 ctlatgaaatggaatgataatgataatgataatgataatgataatgataatgataat 565  
 QY 1071 ACACCTTTGAGCTGCTTCTGGAGAGGCGAATTTACAGTGTGGAGACGATACCTCTTA 1130  
 Db 566 accccctcagactgtctctgagagagagagacaaactccaagggagctccgcaactgccc 625  
 QY 1131 GGTAAACCTTCCTTTGGGTTGGCAAACTTCGACCTTTGGAATTCCTGGAAGATTAAG 1190  
 Db 626 ggcgcgcgagatccagatgagacaaacttgatccagagcagctcgtgagagagctggt 685  
 QY 1191 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1250  
 Db 686 ccccttgcctccctctgagcttccgagag---ctgctagacagagcagagctgagccag 742  
 QY 1251 GGTATCATGAGCGCCCTCTCATATCGCGCCGATCGAGCTGAGCTGAGCTGAGCTGAG 1310  
 Db 743 gctacagtgaggcgcgcctctctgacacacagatgacacacacacacacacacacacac 802  
 QY 1311 AACCAAAATTCACCAACCAACCTCTTTGATTAATTAATTAATTAATTAATTAATTAAT 1370  
 Db 803 aacatcaacagcagagagagctcccaatgctcagagctgagtgagtgagtgagtgag 862  
 QY 1371 TTATCCAGAAAGATATATGACCTGAGAGAGAGAGTGTATTTGGTGGCAGCTCAAGAC 1430  
 Db 863 tctcccaacaaatcactgactgactgagagagatgtgctgagagagatgtgagagac 922  
 QY 1431 AGCACTGGAACACTGCTGACGCGCCATGCCCTGACGACATGTTCCAGTTAATGATGCC 1490  
 Db 923 ccccaagagagctgtctgagagagagagagagagagagagagagagagagagagagag 982  
 QY 1491 AAGCAAAATGACGAGCTCAAGAGGGTACGAGTATGTTCCACATCACTCACTCACTCA 1550  
 Db 983 cgcagctgtaagagatctcggggtgactatcaagacacatgacatgtgtgagtgag 1042  
 QY 1551 GACAAAGCGGACCCATCTCTGAGGCTGAGAGAGAGACATATGAGAGTGTGATCATAG 1610  
 Db 1043 gaggcagcagacacagatgtacaaagcctgtgacagcgcgtctgtgagctgtgccaag 1102  
 QY 1611 AGTGTGACAGAGACACTCAAAAGGTGCTTCTTCCCTGACACACAGCCTGGAGAC 1670  
 Db 1103 ggcctgagcagagagagctccacagcagatcagccttctctccacacacccctgagatac 1162  
 QY 1671 ATCTGAAATCTTCTCTGACAGTCAAGTATCCGCTGGCCAGCGGCTACTTACTCATAG 1730  
 Db 1163 atctgcatgcttctctgaaatgacatgctgacccggtgtgtgagagctatctgcatg 1222  
 QY 1731 CTGCGCTATGCTGCTTATCAATCAATGCTGCTGAGAGCTGCTCAAGTCCAGAGGCTGG 1790  
 Db 1223 ctgacctatgctgtgacacatgctgagtgagagctgagccagctccagaggtctcgtg 1282



OY	373	GGGGGGGCAACATGAGCCCTCCGCTGCTATACGGCCGGCCAGACCCGAGACCGCGCGGGG	432
OY	374	GGGGGGGCAACATGAGCCCTCCGCTGCTATACGGCCGGCCAGACCCGAGACCGCGCGGGG	433
Db	299	gggggggcaacaatgagccctccgctgctatagcgccggccagaccgacggcgggcgggcg	358
OY	433	GCAGCGGCTGTATACGGGTGTCGCCGGAGCGCGCGGTGAGGGCGGAGGGCGCAACAGCAGCG	492
Db	359	gcagcggcctgtatcgtgtgccccggagcgccgctgtgaggggagggcgacacgagcg	418
OY	493	GGGGGCTGGCGCGGTGCTGCTGCGCGCGGACCGGGAGCTATCTGACCGGCCAGCTACTGGC	552
Db	419	ggggggctggcgccgtgtcgtccgagcgagacggagctatctgacccgcccagctactg	478
OY	553	ACGGCGGCTTCGCTCTGAGCAGAGTTTCCAGAGGGGAA	589
Db	479	acgcccgttcgtctgtgagcagatttccaaagtgcga	515
RESULT	15		
ID	V69382	standard; cDNA; 2032 BP.	
XX	V69382;		
XX	01-MAR-1999	(first entry)	
XX	Human Patched-2 cDNA.		
XX	Patched-2; human; patched receptor; diagnosis; disease; screening;		
KW	immune response; immunise; vaccine; inoculation; treatment; cancer;		
KW	kidney diseases; cardiovascular disease; stroke; inflammatory disorder;		
KW	neurological disorder; Alzheimer's disease; Prosis; gene mapping;		
KW	linkage analysis; tissue localisation; ss.		
OS	Homo sapiens.		
PN	EP879888-A2.		
PD	25-NOV-1998.		
XX	20-MAY-1998;	98EP-0303994.	
XX	19-MAR-1998;	98GB-0005954.	
PR	23-MAY-1997;	97GB-0010752.	
XX	(SMIK ) SMITHKLINE BEECHAM PLC.		
XX	Barnes MR, Kelsell DP, Testa TT;		
XX	WPI; 1998-596880/51.		
DR	P-PSDB; W82586.		
PT	New Patched-2 polypeptide and polynucleotide - useful as diagnostic		
PT	reagents and for prevention and treatment of Alzheimer's disease,		
PT	cancer and strokes		
XX	Claim 9b; Page 16-17; 27pp; English.		
PS	This sequence encodes a human patched receptor (Patched-2) polypeptide.		
XX	Patched-2 polypeptides and polynucleotides are useful for diagnosing		
CC	susceptibility to diseases by detecting mutations in the Patched-2 gene		
CC	and can diagnose diseases associated with Patched-2 imbalance. Patched-2		
CC	polypeptides can be used to screen for agonists and antagonists which		
CC	bind the polypeptide by detecting Patched-2 mRNA levels in ELISA assays.		
CC	These can be used in treatment to activate (agonist) or inhibit		
CC	(antagonist) Patched-2 activity. Patched-2 antibodies are useful for		
CC	inducing an immune response to immunise and prevent diseases and for		
CC	isolating Patched-2 clones or purifying the polypeptides by affinity		
CC	chromatography. Patched-2 polypeptides can be administered directly or		
CC	as a vaccine to inoculate against disease. Diseases diagnosed, prevented		
CC	or treated include cancer, kidney disease, cardiovascular disease,		
CC	stroke, inflammatory disorders, neurological disorders including		
CC	Alzheimer's disease and mood disorders and developmental disorders		
CC	including Prosis. The Patched-2 polypeptide is also useful for mapping		

Query Match	8.2%	Score 433.8	DB 19	Length 2032
Best Local Similarity	57.7%	Pred. No. 1.8e+84		
Matches 924	Conservative 0	Mismatches 617	Indels 60	Gaps 6
1958	AGGACAGCAATTAAGAAATCCCTTTTGAGGACAGACCGGGAGTGCCTGAAGCCGACAGG	2017		
Db	33	agggagaagctccccaactctgctctcggcagaagcgcataaggcagtgctctgcagcgacggg	92	
QY	2018	AGCCAGCGCTGGGCCCTCAGCTGCATCAGGAATGTACAGACCTCTTTCATGGCCGCTTAAT	2077	
Db	93	caccegtagtcgaacacacatccataaahaalvgcgccctcccaatgagctgacccctgt	152	
QY	2078	CCCAATTTCCGCTGTCGGGGGTTTCCCTCCGACGACACGGTAGAGTAGTGTTCAATTT	2137	
Db	153	tccatccctcgtgcgcgagcctctccctaaaggcgcataagtgagtgctgctgacctt	212	
QY	2138	TGCCATGCTTCTGCTCATATTTTCTTCGCAATTTCTCAGATTCAGATTTATATGACGGGAGA	2197	
Db	213	tgtaacgctgagctgtctctccagacatcctcagctcagcttaagcgagcgacatg	272	
QY	2198	CAGGAGACTGGAATATTTCTGCTTTTACAAAGCCCTGCGTCAGCAAGATGATTCAGT	2257	
Db	273	ccagcgctctgagtgctgctgctgtctccagctcctgctctgctgagtgatcagat	332	
QY	2258	TGAACCTCAGGCGCTACACGACACACAGACAAATACCCGTACAGCCCCCAACCTCCCTA	2317	
Db	333	ctgtgcccaagg----agctggggagcgggaagatccagtgagcttgcccaactcagt	388	
QY	2318	CAGCAGCCACAGCTTTGCCCATGAAGCCAGATTACCATGCAGTTCACCTGTCCAGTCCG	2377	
Db	389	ccacaggttcaagcctttacc-----cacttgaaagccagcagcagaatgtg	435	
QY	2378	CACGAGTACGACCCCCACACGACGACGTGTACACACACCGCTGAGCGCGTCCGAAAT	2437	
Db	436	gtcacacatctgctcctccccaagcccaactgtagcccccaactctgacccaacttggctct	495	
QY	2438	CTCTGTGCAGCCCGTCACCGTGACAGAGACACCTCAGTTCGACGACCCAGAGACAGC	2497	
Db	496	gagctcttcagccctcgaggaggtgcacaaaggagaccttcaaggccaggag-----gaggag	549	
QY	2498	CAGTCCACAAAGGACGCTCTCTCCAGTTCGCGACTCCACGCTCCACTGCTCTGAGCC	2557	
Db	550	acaagcgagaagcgacg-----ctgcaagtcctc	578	
QY	2558	CCCCGTACGAAGTGGACACCTCTCATCTTTTGTCTAGAAAGCATATGCTCTTTCTCTT	2617	
Db	579	gcccctgtgcccgtgaaatcttgcacatctgcgccgcatacagtltgcccgtgtcgt	638	
QY	2618	GAACCAAAAGCCAAAGGAGTAGTGATATCTCTCTTTCTGCGGCTGCGGGGGTCAAGCT	2677	
Db	639	ccagttcacaaagccaaagccaaatcgtagtgcctcttgtagtctcttcctcggagcttgagct	698	
QY	2678	TTATGGCAACCCGAGTGAGAGAGCGGCTGAGCCTTACGGAATTTGATCTCGGGAAC	2737	
Db	699	ctacggagacacacttgtagcagaagagcctcgtgccccttgagagtgtagtgcctcgggac	758	
QY	2738	CAGAGCAATATGACTTTATGCTGCAACAATTCAATACATTTTCTTCTACACATGTATAT	2797	
Db	759	caagagatgctcctctcgaagcgcccaagctcagtaacttccctgtacgagtggtgcct	818	
QY	2798	AGTCCCAAGAAAG---CAGACTACCCGGAATTCAGGACTTACCTTACGACTTCACAG	2854	
Db	819	gtgtgcccaaggtgctttagactacgcccactcccaagcgccctctttagcttgacaca	878	
QY	2855	GAGTTTCAGTAACTGGAAGTATGTATGTGTGGAAAGAAACAAACAGCTTCCCAAAATGTG	2914	

```
Db 879 ggccttcagltccctcaaggcgglycctgcacccacccgacccagccacccgcacccctg 938
QY 2915 GCTGCACACTACTTACAGAGACTGGCTTCAGGACTTCAGGATTCATTGTGACACTGAGGA 2974
Db 939 gctgcactataccgcacacgcgtctacaggaatcccaagctgccttgaaccaagacatgggc 998
QY 2975 AACCGGGAAATCATGGCAAAACATTACAAGATGATCAGACGATGAGTCTTGCCCTA 3034
Db 999 tcttggtgcgtacaccgcacccgtacccaatgctctgagatggtggccctggccta 1058
QY 3035 CAAACTCCTTGCTGCAAAACCCGACCCGATTAAGCCCATGACATCAGCCGTTGACTTA 3094
Db 1059 caagctgcctacccacacacgagacgcccagagcctctggaatctcagccagctgaaccac 1118
QY 3095 ACAGCCTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3154
Db 1119 aaggaaagcttggtgacagaaagagactgattccaccgagctcttcaatgggctgagc 1178
QY 3155 GGCCTGGGTCAGCAACGACCCGCTCGGATGCTGCTCCAGGCAACATCCGGCCACA 3214
Db 1179 cgtgtgtgtgagcagtgagccctggctcgtgcagcctcaagcacaactctacccccc 1238
QY 3215 CCGACCAAGATGGGTCACACCAAAAGCCGACTACATGCTGAACAAGCTGAGATCC 3274
Db 1239 acctcctgaatggctgacagacaatacgaacacacgagggagagac---cttcgcatccc 1295
QY 3275 GGCACGAGAGCCCATGAGATGAGCCGCTCCCTTCCTTACCTCAACGGGTTGGGGACAC 3334
Db 1296 gccaagctcagccttgagaglttgccagctcccttccctcgtcgtgcctccagaagac 1355
QY 3335 CTCAGACTTTGTGAGAGCAATTGAAAAAGTAAAGACCATCTGACGAACATATACGAGCCT 3394
Db 1356 tgcagacctgtgtgagagccatcgaggggcccggcagcatgcccagagggccggccaggc 1415
QY 3395 GGGGCTGTCCAGTTACCCCAACGGCTACCCCTTCCTCTTGAGGACGATACATGGGCT 3454
Db 1416 tgggggtgcaagcctaccacagcggctcccttcccttctcttggaacaglatctgggcct 1475
QY 3455 CCGCCACTGAGCTGCTGCTGTTTCATCAACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3514
Db 1476 gctggcgtcgtcctcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1535
QY 3515 TGTCTTCCTTGTGAACCCCTGGAAGGCGGAGATCATTTGTGA 3555
Db 1536 tctgtcgtcctcctcaccctctgagtgtgctggcctcatagtaga 1576
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Search completed: January 13, 2001, 09:23:41  
Job time: 1159 sec

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:14:57 ; Search time 116.97 Seconds  
(without alignments)  
7285.763 Million cell updates/sec

Title: US-08-656-055-18

Perfect score: 5288

Sequence: 1 GAATTCGGGACCGCAAGG.....TATGAAGAAAGCCCGGAATT 5288

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 280836 segs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/prodata/2/lna/5A\_COMB.seq:\*  
2: /cgn2\_6/prodata/2/lna/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/2/lna/6\_COMB.seq:\*  
4: /cgn2\_6/prodata/2/lna/PCrUS\_COMB.seq:\*  
5: /cgn2\_6/prodata/2/lna/backfileseq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5288	100.0	5288	2	US-08-540-406-18
2	5288	100.0	5288	3	US-08-656-055-18
3	5288	100.0	5288	4	US-08-540-406-18
4	3801.2	71.9	5187	2	US-08-540-406-3
5	3801.2	71.9	5187	2	US-08-540-406-9
6	3801.2	71.9	5187	3	US-08-656-055-3
7	3801.2	71.9	5187	3	US-08-656-055-9
8	3801.2	71.9	5187	4	US-08-540-406-3
9	3801.2	71.9	5187	4	US-08-540-406-9
10	411.8	7.8	3900	2	US-08-356-0608-42
11	411.8	7.8	3900	2	US-08-460-900C-42
12	405	7.7	4434	2	US-08-540-406-5
13	405	7.7	4434	3	US-08-656-055-5
14	405	7.7	4434	4	US-08-540-406-7
15	405	7.7	4434	4	US-08-540-406-7
16	77	1.5	345	2	US-08-656-055-7
17	77	1.5	345	4	US-08-656-055-7
18	67.6	1.3	4524	2	US-08-656-055-7
19	67.6	1.3	4524	2	US-08-656-055-7
20	66.6	1.3	4524	2	US-08-656-055-7
21	66.6	1.3	4524	2	US-08-656-055-7
22	66.6	1.3	4524	2	US-08-656-055-7
23	64.8	1.2	8438	1	US-08-540-406-1
24	61	1.2	397	3	US-08-540-406-1
25	60.8	1.1	6530	2	US-08-146-930-1
26	60.8	1.1	6530	2	US-08-146-930-1
27	60.8	1.1	6530	4	US-08-458-240-1
28	60.4	1.1	5115	3	US-08-348-518C-3

C 29	60.4	1.1	5115	3	US-08-476-509B-3	Sequence 3, Appl1
C 30	58.8	1.1	5288	2	US-08-540-406-18	Sequence 18, Appl1
C 31	58.8	1.1	5288	3	US-08-656-055-18	Sequence 18, Appl1
C 32	58.8	1.1	5288	4	US-08-557-309B-18	Sequence 18, Appl1
C 33	57.6	1.1	1235	2	US-08-834-306-15	Sequence 15, Appl1
C 34	57.6	1.1	1235	2	US-08-834-306-15	Sequence 15, Appl1
C 35	57.4	1.1	530	3	US-08-758-662-4	Sequence 4, Appl1
C 36	57.4	1.1	4257	2	US-08-690-473-1	Sequence 1, Appl1
C 37	57.4	1.1	5117	3	US-08-854-585-1	Sequence 1, Appl1
C 38	57.4	1.1	5117	4	US-08-854-585-1	Sequence 1, Appl1
C 39	57.4	1.1	12001	1	US-08-458-568B-11	Sequence 11, Appl1
C 40	56.8	1.1	234	1	US-08-469-802B-3	Sequence 3, Appl1
C 41	56.8	1.1	234	2	US-08-267-802B-3	Sequence 3, Appl1
C 42	56.8	1.1	2823	1	US-08-398-008A-1	Sequence 1, Appl1
C 43	56.8	1.1	2823	2	US-08-893-333-1	Sequence 1, Appl1
C 44	56.4	1.1	2538	3	US-08-899-437-1	Sequence 1, Appl1
C 45	56.4	1.1	10348	2	US-08-457-273B-41	Sequence 41, Appl1

## ALIGNMENTS

RESULT 1  
US-08-540-406-18  
; Sequence 18, Application US/08540406  
; Patent No. 5837538  
; GENERAL INFORMATION:  
; APPLICANT: SCOTT, MATHEW P  
; APPLICANT: GOODRICH, LISA V  
; APPLICANT: JOHNSON, RONALD L  
; TITLE OF INVENTION: Patched Genes and their use  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/540,406  
; FILING DATE: 06-OCT-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertram I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: a60190-1  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5288 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-540-406-18

Query Match 100.0%; Score 5288; DB 2; Length 5288;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGACCGCAAGAGTGGCGGGAAGCGCCGGAAGAGACGCTCGCGGCG 60  
DB 1 GAATTCGGGACCGCAAGAGTGGCGGGAAGCGCCGGAAGAGACGCTCGCGGCG 60

QY	61	GC	GGCTCTCGCTCTTC	CGGCAACTG	GAATG	GGGAG	CGGGG	CGGCA	GAACCTTG	GGGA	120
Db	61	GC	GGCTCTCGCTCTTC	CGGCAACTG	GAATG	GGGAG	CGGGG	CGGCA	GAACCTTG	GGGA	120
QY	121	CCCCGCGCA	ATGTTGGCA	TGGAAGCG	AGGGTCT	GACTTCC	CCGGC	ACGCG	CGCGGC	980	
Db	121	CCCCGCGCA	ATGTTGGCA	TGGAAGCG	AGGGTCT	GACTTCC	CCGGC	ACGCG	CGCGGC	980	
QY	121	CCCCGCGCA	ATGTTGGCA	TGGAAGCG	AGGGTCT	GACTTCC	CCGGC	ACGCG	CGCGGC	980	
Db	121	CCCCGCGCA	ATGTTGGCA	TGGAAGCG	AGGGTCT	GACTTCC	CCGGC	ACGCG	CGCGGC	980	
QY	181	GC	AGGGGCA	GCAGCGCCCG	CGCTGT	GAGAG	AGCAGCGCCG	CTGTGT	CAACCCG	AGGC	240
Db	181	GC	AGGGGCA	GCAGCGCCCG	CGCTGT	GAGAG	AGCAGCGCCG	CTGTGT	CAACCCG	AGGC	240
QY	241	CG	AGCCCG	AGAGCAGCT	GTGGG	CCAGAG	AGCGCT	CCAGCG	CGCCAG	300	
Db	241	CG	AGCCCG	AGAGCAGCT	GTGGG	CCAGAG	AGCGCT	CCAGCG	CGCCAG	300	
QY	301	CAG	CCCCG	CAGCAGCGG	CAGCAGCGG	CGCCG	CGCCG	CGGAA	CGCTTCC	CGCGG	360
Db	301	CAG	CCCCG	CAGCAGCGG	CAGCAGCGG	CGCCG	CGCCG	CGGAA	CGCTTCC	CGCGG	360
QY	361	CG	CGCGG	CGCGCGG	CGCGC	CAACAT	TGGCTTG	TAA	CGCGCGG	CGCAG	420
Db	361	CG	CGCGG	CGCGCGG	CGCGC	CAACAT	TGGCTTG	TAA	CGCGCGG	CGCAG	420
QY	421	CG	CGCGG	CGCGCGG	CGCGC	CAACAT	TGGCTTG	TAA	CGCGCGG	CGCAG	480
Db	421	CG	CGCGG	CGCGCGG	CGCGC	CAACAT	TGGCTTG	TAA	CGCGCGG	CGCAG	480
QY	481	CG	AGAGCG	AGAGCGG	GGGCG	GTGGCG	CGCGCGG	CGCGG	AGCACT	ATCTCAC	540
Db	481	CG	AGAGCG	AGAGCGG	GGGCG	GTGGCG	CGCGCGG	CGCGG	AGCACT	ATCTCAC	540
QY	541	CC	AGCTACT	CGCAGCGCG	CTTCG	CTCTG	AGAGAGAT	TTTCA	AGGGG	GAAGCTACT	600
Db	541	CC	AGCTACT	CGCAGCGCG	CTTCG	CTCTG	AGAGAGAT	TTTCA	AGGGG	GAAGCTACT	600
QY	601	GGA	AGCGCG	CACTGT	GGCTG	AGAGG	CGCA	GTTCAG	AGACTCT	ATTTAA	660
Db	601	GGA	AGCGCG	CACTGT	GGCTG	AGAGG	CGCA	GTTCAG	AGACTCT	ATTTAA	660
QY	661	ACA	TTTCAAAAAA	AACTCGCG	CAATTTGG	TGGG	CCCTCA	ATTTG	GGGCG	CTTCG	720
Db	661	ACA	TTTCAAAAAA	AACTCGCG	CAATTTGG	TGGG	CCCTCA	ATTTG	GGGCG	CTTCG	720
QY	721	CG	GTGGG	ATTTAA	AGCAGC	GAACCTG	AGACCA	CACTG	GGAGG	AGCTGGG	780
Db	721	CG	GTGGG	ATTTAA	AGCAGC	GAACCTG	AGACCA	CACTG	GGAGG	AGCTGGG	780
QY	781	GAG	GAGAG	GAGTAA	GTG	TGAATTA	TACTG	CGCA	GAAAGATTG	GGAAGAG	840
Db	781	GAG	GAGAG	GAGTAA	GTG	TGAATTA	TACTG	CGCA	GAAAGATTG	GGAAGAG	840
QY	841	TTA	TATCTCA	CTCAT	GATGAT	CAGAC	CCCTTAA	AGAA	GAGTGT	ATGTCTG	900
Db	841	TTA	TATCTCA	CTCAT	GATGAT	CAGAC	CCCTTAA	AGAA	GAGTGT	ATGTCTG	900
QY	901	AA	CGGCG	CTCA	CAACACT	GTG	AGCAG	CACTG	CAAGCG	CACTGTG	960
Db	901	AA	CGGCG	CTCA	CAACACT	GTG	AGCAG	CACTG	CAAGCG	CACTGTG	960
QY	961	ACA	ACAGG	CGATG	GAATTTG	GAACAT	TTTGT	TACAA	TATCAG	GAGACCTT	1020
Db	961	ACA	ACAGG	CGATG	GAATTTG	GAACAT	TTTGT	TACAA	TATCAG	GAGACCTT	1020
QY	1021	CAG	GTTA	CAATG	ATGATTA	TGAATAT	TTTAC	CTTG	TGATTA	TTTAC	1080
Db	1021	CAG	GTTA	CAATG	ATGATTA	TGAATAT	TTTAC	CTTG	TGATTA	TTTAC	1080
QY	1081	ACT	GCTTCT	TGGA	AGGGCG	CAATTTAC	AGTCTG	GGAG	ACAT	ACTCT	1140
Db	1081	ACT	GCTTCT	TGGA	AGGGCG	CAATTTAC	AGTCTG	GGAG	ACAT	ACTCT	1140
QY	1141	CTT	TGCGGTG	ACAACTT	CGACCTT	TGGAATTT	CCTG	GAAG	AGTTAA	AGAAATTA	1200

Db	1141	CTTTCGGGTGGACAACCTTCGACCCTTTTGAAATTCCTGGAAAGTAAAGAAATTAACCT	1200
QY	1201	ATCAAGTGGACAGCTGGGAGGAAATGCTGAAATAAGGCTGAGGTGGTCAATGGTACATAG	1260
Db	1201	ATCAAGTGGACAGCTGGGAGGAAATGCTGAAATAAGGCTGAGGTGGTCAATGGTACATAG	1260
QY	1261	ACCGCCCTGCGCTCAATCCGGCCGATTCAGACTGCCCCCACCAGCCCAACAAAAAT	1320
Db	1261	ACCGCCCTGCGCTCAATCCGGCCGATTCAGACTGCCCCCACCAGCCCAACAAAAAT	1320
QY	1321	CAACCAAACTTGTATATGCGCTTGTTTTGAATGTTGGATGTCATGGCTTATCCAGA	1380
Db	1321	CAACCAAACTTGTATATGCGCTTGTTTTGAATGTTGGATGTCATGGCTTATCCAGA	1380
QY	1381	AGTATATGACTGGCAGAGAGATTGATGTTGGTGGCCAGTCAAGAACAGCACTGGAA	1440
Db	1381	AGTATATGACTGGCAGAGAGATTGATGTTGGTGGCCAGTCAAGAACAGCACTGGAA	1440
QY	1441	AACTCGTCAGGCGCCATGSCCTGACAGACATGTTCCAGTTAATGACTCCCAAGCAATGT	1500
Db	1441	AACTCGTCAGGCGCCCATGSCCTGACAGACATGTTCCAGTTAATGACTCCCAAGCAATGT	1500
QY	1501	ACGAGCACTCAAGGGGTACGAGTATGTCACACATCAACTGAAGAGAGCAAAAGCG	1560
Db	1501	ACGAGCACTCAAGGGGTACGAGTATGTCACACATCAACTGAAGAGAGCAAAAGCG	1560
QY	1561	CAGCATTCTGAGGCGCTGGCAGAGACATATGTGAGAGTGGTGTTCATCAGAGTGTGAC	1620
Db	1561	CAGCATTCTGAGGCGCTGGCAGAGACATATGTGAGAGTGGTGTTCATCAGAGTGTGAC	1620
QY	1621	AGACATCCACTCAAAAGGTGCTTCTCTACACACACAGACCCGAGAGACATCTGAAAT	1680
Db	1621	AGACATCCACTCAAAAGGTGCTTCTCTACACACACAGACCCGAGAGACATCTGAAAT	1680
QY	1681	CCATTCTACGCTACATGTCATCCGGTGGCCAGCGCTACTTACTCATGCTGCGCTATG	1740
Db	1681	CCATTCTACGCTACATGTCATCCGGTGGCCAGCGCTACTTACTCATGCTGCGCTATG	1740
QY	1741	CGTGTTAACATGCTGCGCTGGGACTGCTGTCCAAGTCCAGAGGTCGCCGTGGGCTGGCTG	1800
Db	1741	CGTGTTAACATGCTGCGCTGGGACTGCTGTCCAAGTCCAGAGGTCGCCGTGGGCTGGCTG	1800
QY	1801	GGCTTCGCTGGGTGACACTGTCAGTGGCTCAGAGACTGGGCTCTGTGCTCATTTATCGGA	1860
Db	1801	GGCTTCGCTGGGTGACACTGTCAGTGGCTCAGAGACTGGGCTCTGTGCTCATTTATCGGA	1860
QY	1861	TTTCTTTAAACGTCGACACTCAGGTTTGGCATTTCCTGCTCTTGGTGGTGGTGG	1920
Db	1861	TTTCTTTAAACGTCGACACTCAGGTTTGGCATTTCCTGCTCTTGGTGGTGGTGG	1920
QY	1921	ATGATGTTTTTCTTGGCCACGCGCTTACGTAAACAGAGACAGAAATAAAGATCCCT	1980
Db	1921	ATGATGTTTTTCTTGGCCACGCGCTTACGTAAACAGAGACAGAAATAAAGATCCCT	1980
QY	1981	TTGAGGACAGACCGGGAGATGCTGTGAAGCGACAGAGCCAGCGTGCGCTCAGCTCA	2040
Db	1981	TTGAGGACAGAGCCGGGAGATGCTGTGAAGCGACAGAGCCAGCGTGCGCTCAGCTCA	2040
QY	2041	TCAGCAATGTCACAGCCTTCTCATGGCCGCGTTAATCCCAATCCCGCTCGGGGCGT	2100
Db	2041	TCAGCAATGTCACAGCCTTCTCTATGGCCGCGTTAATCCCAATCCCGCTCGGGGCGT	2100
QY	2101	TCGCCCTCCAGGACGGGTAGTGTGTCTCAATTTTGGCATGTTCTGCTCAATTTTC	2160
Db	2101	TCGCCCTCCAGGACGGGTAGTGTGTCTCAATTTTGGCATGTTCTGCTCAATTTTC	2160
QY	2161	CTGCAATTTCTCAGATGATTTATATGACGCGAGACAGAGACATGATATTTCTGCT	2220
Db	2161	CTGCAATTTCTCAGATGATTTATATGACGCGAGACAGAGACATGATATTTCTGCT	2220
QY	2221	GTTTTCACACCCCTGGGTGAGAGATGTGATTCGTTGAACCTCAGGCTCACCGACA	2280
Db	2221	GTTTTCACACCCCTGGGTGAGAGATGTGATTCGTTGAACCTCAGGCTCACCGACA	2280



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Db 2221 GTTTACAAGCCCTGCGTCAGACAGATGATTGACCTGAGCCCTACACCGACA 2280
Qy 2281 CACACGACAAATACCCGCTACAGACCCCCACCTCCCTACAGACAGCCACAGTTTGCCATG 2340
Db 2281 CACAGACAAATACCCGCTACAGACCCCCACCTCCCTACAGACAGCCACAGTTTGCCATG 2340
Qy 2341 AAGGCAATTAACCATGAGTCCACTGTCCACTCCGACGAGATGACACCCACACGC 2400
Db 2341 AAGGCAATTAACCATGAGTCCACTGTCCACTCCGACGAGATGACACCCACACGC 2400
Qy 2401 ACCTGTACTACACACCCGCTGAGCCGCTCCGAGATCTCTGAGAGCCGCTACACGTA 2460
Db 2401 ACCTGTACTACACACCCGCTGAGCCGCTCCGAGATCTCTGAGAGCCGCTACACGTA 2460
Qy 2461 CACAGACACCCCTACGCTGAGAGCCACAGAGACACGATCCACAAAGGACCTGCTG 2520
Db 2461 CACAGACACCCCTACGCTGAGAGCCACAGAGACACGATCCACAAAGGACCTGCTG 2520
Qy 2521 CCCAGTCTCCGAGCTCCGAGCCCTCCGCTGAGAGCCGCTCCGAGATCTCTGAGAG 2580
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Db 2641 TGATCTTCCTTTTCTGGGCTTCTGCTGGGGGTACGCTTTATGAGCACCCGAGTAG 2700
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Db 2701 ACGGGCTGAGACCTTACGAGCATTTGACTGGGAAACAGAGAAATATACCTTATGCTG 2760
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Db 2761 CACAAATCAAAATCTTTTCTTACAAACATGATATATAGTACACCCAGAAAGAGACTAC 2820
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Db 2821 CGAATATCCAGACCTTACTTACGACCTACACAGAGATTTAGTAACCTGAAATGTCGA 2880
Qy 2881 TGTGGAAGAAACAAACAGCTTCCCAAAATGTGGCTGACTACTTTCAGAGCTGGCTTC 2940
Db 2881 TGTGGAAGAAACAAACAGCTTCCCAAAATGTGGCTGACTACTTTCAGAGCTGGCTTC 2940
Qy 2941 AGGAGCTTCAGGATGCAATTTGACAGTACGTGGAACCGGGAATATGCCAAACAAAT 3000
Db 2941 AGGAGCTTCAGGATGCAATTTGACAGTACGTGGAACCGGGAATATGCCAAACAAAT 3000
Qy 3001 ACAGAATGATATGAGAGATGAGTCTGCTGCTACAAACCTGCTGCTGCTGCTGCTGCT 3060
Db 3001 ACAGAATGATATGAGAGATGAGTCTGCTGCTACAAACCTGCTGCTGCTGCTGCTGCT 3060
Qy 3061 GCGATTAAGCCCATGACATGAGCCAGTTGACTAAACAGCGCTGCTGCTGCTGCTGCTG 3120
Db 3061 GCGATTAAGCCCATGACATGAGCCAGTTGACTAAACAGCGCTGCTGCTGCTGCTGCTG 3120
Qy 3121 TCATTAATCCAGCGCTTTTATACATGATGATGAGCGCTTGGGTGACAGACGCCCTGCG 3180
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Qy 3181 CGTATGCTGCTCCAGGCGCAACATCGGCGCACACGACAGAGATGGGTCCAGACAAAG 3240
Db 3181 CGTATGCTGCTCCAGGCGCAACATCGGCGCACACGACAGAGATGGGTCCAGACAAAG 3240
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Db 3241 CCGAGCTACATGCTGTAACAGGCTGAGAAATCCCGGAGAGAGAGCCCATGAGTATGCC 3300
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Qy 3361 AAGTAAGACCATCTGACGACACTATAGAGAGCTGGGCTGTCCAGTTAACCCAAAGGCT 3420
Db 3361 AAGTAAGACCATCTGACGACACTATAGAGAGCTGGGCTGTCCAGTTAACCCAAAGGCT 3420
Qy 3421 ACCCTTCTCTTCTGGAGAGATACATGGGCTCCGACAGCTGGCTGGCTGGCTGATCA 3480
Db 3421 ACCCTTCTCTTCTGGAGAGATACATGGGCTCCGACAGCTGGCTGGCTGGCTGATCA 3480
Qy 3481 GCGTGTGTGGCTGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Db 3481 GCGTGTGTGGCTGCAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3540
Qy 3541 CCGGATCATTTGATGATGCTGGGCTGGGCTGATGAGAGCTGTGCGCATATGGGCC 3600
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Qy 3601 TCATCGGAATCAAMGCTAGTCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3660
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Qy 3661 GAGTGGAGTTACCCCTTCACGTTGCTTGGCTTGTGACGGCATCGGCAAGAAC 3720
Db 3661 GAGTGGAGTTACCCCTTCACGTTGCTTGGCTTGTGACGGCATCGGCAAGAAC 3720
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Db 3721 GCAGGGCTGTGCTTGGCTGAGACATGTTTGCACCCGCTGCTGCTGCTGCTGCTGCTGCT 3780
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Qy 3961 TGGCCACACCTTCCCTGAGCCACCCCGACAGCGTGGCTGCTGCTGCTGCTGCTGCTGCT 4020
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Qy 4081 GCCTCAGCAGAGAGCTTGGCACTAGAGGCGCCAGCAGGCGCGGAGGCGCTGCGCAC 4140
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Qy 4321 CACCCCTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4380
Db 4321 CACCCCTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4380
Qy 4381 CTAGCAATAGGGCGCTGGGGCGCTGGGGCGCTGCTGACAAACCTCGGAACCCAG 4440
Db 4381 CTAGCAATAGGGCGCTGGGGCGCTGGGGCGCTGCTGACAAACCTCGGAACCCAG 4440

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QY 4441 CTTCCACTGCGATGGAGCTCCCTGCCGCTACTGCGACGCCATCCACTGAGGG 4500  
 DB 4441 CTTCCACTGCGATGGAGCTCCCTGCCGCTACTGCGACGCCATCCACTGAGGG 4500  
 QY 4501 CTTCTGCTCCGTCAGTGTGCGCCCTGACACCGCCGCTGCTGCGGCTGGGCGAAC 4560  
 DB 4501 CTTCTGCTCCGTCAGTGTGCGCCCTGACACCGCCGCTGCTGCGGCTGGGCGAAC 4560  
 QY 4561 CCGGAGGGGAGCTCTGCGGAGCTACCTGAGACTGACACGCGCTGTTGAGACCC 4620  
 DB 4561 CCGGAGGGGAGCTCTGCGGAGCTACCTGAGACTGACACGCGCTGTTGAGACCC 4620  
 QY 4621 ACCTGCTTCCAGCTCCGCTGCTGAGAGGAGGATTCAGAGTGGAGCATTTGAGCTCC 4680  
 DB 4621 ACCTGCTTCCAGCTCCGCTGCTGAGAGGAGGATTCAGAGTGGAGCATTTGAGCTCC 4680  
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 DB 4681 AGGACGTGAGATGGAGAGAGGCGCGGAGAGGAGCTCCAGCTGAGGGTGAATTAAT 4740  
 QY 4741 CTGAGAGAGAGGCGCAAGATTTGAGAAACCCCGACCCCGCTCTTCCAGACTGCTT 4800  
 DB 4741 CTGAGAGAGAGGCGCAAGATTTGAGAAACCCCGACCCCGCTCTTCCAGACTGCTT 4800  
 QY 4801 GAAGAGAACTGCTGAGCTTATGAGAAAGATCCCTGTCAGAGAGAGCTTCATTTGT 4860  
 DB 4801 GAAGAGAACTGCTGAGCTTATGAGAAAGATCCCTGTCAGAGAGAGCTTCATTTGT 4860  
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 DB 4861 ACTGTAAACGATTTGATTTATTTTGTAAATATTTCTATTAATATTTAGAGATGTAACA 4920  
 QY 4921 TGTGTAAATATGAGAGAGAGATGTAAGTGTATGATCTGGGGCTTCCACTGCTGCC 4980  
 DB 4921 TGTGTAAATATGAGAGAGAGATGTAAGTGTATGATCTGGGGCTTCCACTGCTGCC 4980  
 QY 4981 CCAGAGTGTGAGGCGCAAGAGTGGGCGCTCTCCGATTTTGTGAGTGGGCTCCGTCGACA 5040  
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 QY 5041 ACCAAGCTTCAATTAATTTTCAAGATTTGTTGCTGCTGCTTAATTTGTTAAT 5100  
 DB 5041 ACCAAGCTTCAATTAATTTTCAAGATTTGTTGCTGCTGCTTAATTTGTTAAT 5100  
 QY 5101 TTACTGTATATTTCTATGCAAAATTTGCTTAATAGATTTATTTGTAAGCTTTC 5160  
 DB 5101 TTACTGTATATTTCTATGCAAAATTTGCTTAATAGATTTATTTGTAAGCTTTC 5160  
 QY 5161 TGTTTAAATATTTTAAATTTGCATATTCACAAACCTGTGTAGTATGAATTTACTGTT 5220  
 DB 5161 TGTTTAAATATTTTAAATTTGCATATTCACAAACCTGTGTAGTATGAATTTACTGTT 5220  
 QY 5221 AACTTTCAAAACGCTATGCGTATGATTAATTTTGTATATGAGATTTGAAGAAC 5280  
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 QY 5281 CCGGAAAT 5288  
 DB 5281 CCGGAAAT 5288

# RESULT 2 US-08-656-055-18.

; Sequence 18, Application US/08656055  
 ; Patent No. 6027862  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SCOTT, MATHEW P  
 ; APPLICANT: GOODRICH, LISA V  
 ; APPLICANT: JOHNSON, RONALD L  
 ; TITLE OF INVENTION: Patched Genes and their Use  
 ; NUMBER OF SEQUENCES: 19  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400  
 ; CITY: San Francisco  
 ; STATE: CA  
 ; COUNTRY: US  
 ; ZIP: 94111  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/656,055  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/540,406  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Rowland, Bertram I  
 ; REGISTRATION NUMBER: 20015  
 ; REFERENCE/DOCKET NUMBER: a60190-1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-781-1989  
 ; TELEFAX: 415-398-3249  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 5288 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-656-055-18

Query Match 100.0%; Score 5288; DB 3; Length 5288;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 GCGGCTCTGCTTCTCCGCACTGATGTTGGGAGGGGCGCGGAGAGCTCGGGA 120  
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 DB 121 CCCCCGGCAATGAGCAATGGAAGGCGCAGGGTGTGACTCCCGGAGCGCGCGGC 180  
 QY 181 GCAGCGGAGAGAGCGCGCGCGTGTGAGCAGCAGCGGCTGTCTGCAACCGGAGCC 240  
 DB 181 GCAGCGGAGAGAGCGCGCGCGTGTGAGCAGCAGCGGCTGTCTGCAACCGGAGCC 240  
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 DB 301 GAGCGCGGAGAGAGCGCGCAGCAGCGCGCGCGCGGAGAGCTTCCGCGCGCGG 360  
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 DB 361 GCGGCGGCGGCGGCGGCGGCAACATGAGCTGCTGTTAAACCGCGGAGCGGAGGAC 420  
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 DB 421 GCGGCGGCGGCGGCGGCGGCTATCGGTGCCCCGAGAGCGCGGCTGAGAGCGGAGG 480  
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 DB 481 GCAGCGAGAGGAGGAGGCTGCGCGTGTGCTGCGCGCGGAGCGGAGCTATCTGACACGG 540

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# RESULT 3 PCT-US95-13233-18

; Sequence 18, Application PC/TUS9513233

; GENERAL INFORMATION:

; APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY

; TITLE OF INVENTION: Patched Genes and their Use

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS: Flehr, Hohbach, Tesl, Albrighton & Herbert

; ADDRESS: Four Embarcadero Center, Suite 3400

; City: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/13233

; FILING DATE: 06-OCT-1990

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertam I

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: a60190-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5288 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: CDNA

; PCT-US95-13233-18

Query Match 100.0%; Score 5288; DB 4; Length 5288;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 5281 CCGGAATP 5288

RESULT 4  
 US-08-540-406-3  
 ; Sequence 3, Application us/08540406  
 ; Patent No. 5837538  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SCOTT, MATHEW P  
 ; APPLICANT: GOODRICH, LISA V

```

APPLICANT: JOHNSON, RONALD L
TITLE OF INVENTION: Patched genes and their use
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,406
FILING DATE: 06-OCT-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: a60190-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5187 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-540-406-3

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Query Match 71.9%; Score 3801.2; DB 2; Length 5187;

Best Local Similarity 88.1%; Pred. No. 0; Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

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[illegible]

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RESULT 7
US-08-656-055-9
: Sequence 9, Application US/08656055
: Patent No. 602/882
: GENERAL INFORMATION:
: APPLICANT: SCOTT, MATHEW P
: APPLICANT: GOODRICH, LISA V
: APPLICANT: JOHNSON, RONALD L
: TITLE OF INVENTION: Patched Genes and their use
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
: STREET: Four Embarcadero Center, Suite 3400
: CITY: San Francisco
: STATE: CA
: COUNTRY: US
: ZIP: 94111
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/656,055
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/540,406
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Rowland, Bertram I
: REGISTRATION NUMBER: 20015
: REFERENCE/DOCKET NUMBER: a60190-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-781-1989
: TELEFAX: 415-398-3249
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5187 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-656-055-9

Query Match 71.9%; Score 3801.2; DB 3; Length 5187;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

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506 TGTCTGCGCGCGCGGAGACCGCGGAGCTATCTCACCAGGCGCCAGCTACTGCGACGCCGCTTGGC 565

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Db	3357	TTTGGCTTTTTCAGACGCAATTTGGGGACAAAGAACAGGGCTGTATGCTGCTGGAAACA	3416
QY	3746	CATGTTTCCACCCGTCCTGGATGAGCGCGCTGTGCCACTGCTGGGAGTGCCTATGCTGCG	3805
Db	3417	CATGTTTCTCCCGCTTTCGGAGCGGTGTGTGCCACTGTGCTGGGCTGTACTATGCTTTC	3476
QY	3806	GGGATCTAGATTTCGACTTCATTTGTAGGTATTTCTTTGCTGTGCGGAGCTTCACAT	3865

Db	3477	AGGGTCGAAATTTGATTTCAATGTTCAGAACTCTTTGGCGTCCCTGCTTTGCTTTGCTTTGACACATA	353
Qy	3866	CCTGGCGCTTCTCAATGGGGTGGTWTTCCTCCGTCCTTTGCTTTGCTTTGACACATA	392
Db	3537	CTTGGGGGTTCTCAATGACTGGTCTCTGCTGCTCTCCCTCTTATCCTTTCTTTGGACCGTG	359
Qy	3926	TCTGAGGTGCTCCAGCCAAAGGCTTAAACGGCTGGCCACACCCTCCCTGAGCACC	398
Db	3597	TCTGAGGTGCTCCAGCCAAAGGCTTAAACGGCTGGCCACACCCTCCCTGAGCACC	365
Qy	3986	CCCCAGCGTGGTCCGCTTCCGCTATGCCGCCCGGCCACACAGCACAGGGTCTGATTCCTC	404
Db	3657	TCCAAGTGTGCTCGGTTTGGCTGGTCCCTGATGTCACACGAACATAGGTCTGATTCCTC	371
Qy	4046	CGACTCGGAGTATGTTCCCGACGACAGTGTCAAGCCTCAAGGAGACCTTGGCCTATA	410
Db	3717	CGACTCGGAGTATGTTCCCGACGACAGTGTCTGGCATCAGTGGAGTCTCAGCCATA	377
Qy	4106	CGAGGCCACGAGGAGCGGGAGGCGCCGCCACCAACTGATTCGGAAGCCACAGAAA	416
Db	3777	CGAAGCACAGAGGGTCCGGAGGCGCTGCCACCAAGTATGTTGGAAAGCCACAGAAA	383
Qy	4166	CCCCGTTTGGCCACTCTCACTGTGTGCATCCGAATCCAGGATCAACCCCTCGAA	422
Db	3837	CCCCGTTTGGCCGCTTCCACTGTGTGCATCCGGAATCCAGATCAAGCTCCCTTAC	389
Qy	4226	CCCGAGCAGACAGCCGACCTGAGACTCAGGGTCCCTGCTCCCGAGCGCAAGCCACGA	428
Db	3897	CCCTCGCAACAGCCCACTCGACTCTGTCTTGTCCCTGGACGCAAGGCAACGA	395
Qy	4286	GCCCCGAGGAGACCCCCACAGAGAAAGCTTGTGGCCACCCCTTACACAGCGCGAGAGA	434
Db	3957	GCTTCGAAGGATCCCTTAGAGAAAGGCTTGGGCGACCCCTTACACAGCGCGAGAGA	401
Qy	4346	CGCTTTTGAATTTCTACTGAAGGGCAATTCTGGCCCTAGCAATAGGGCCGCTGGGGCC	440
Db	4017	CGCTTTTGAATTTCTACTGAAGGGCAATTCTGGCCCTAGCAATAGGGCCGCTGAGGCC	407
Qy	4406	TCCGCGGGGCCGTTTCTCACAACTTCGGAACCCAGCGTCCACTGCATAGGGGAGCTCCGT	446
Db	4077	CGTGGGGGCCGTTTCTCACAACTTCGGAACCCAGCGTCCACTGCATAGGGGAGCTCTGT	413
Qy	4466	GCCCCGCTACTCCAGCCCACTCACACTGTGACGGCTTGTGCTCCGTGACTGTGCGCGT	452
Db	4137	GCCCCGCTACTCCAGCCCACTCACACTGTGACGGCTTGTGCTCCGTGACTGTGCGCGT	419
Qy	4526	GCACCGCGCGCTGTCCCTGGGGCTGGGGCGGAACCCCGAGGGGAGCTCTGCCAG----	458
Db	4197	GCATCCCCCG-----CTGGACCTGGGGCGGAACCCCGAGGGGCGCTCTCAAGGCTA	425
Qy	4582	-----GCTACCCCTGAGACTGACACAGCGCTGTGTGAGAGACCCCGACGTCCTTTCACGT	463
Db	4251	TGAGAGCTACCTCGAAGACTGATCAGGGGGATTTTGAAGATTCATATGCTTTTCAATGT	431
Qy	4637	CCGGTGTGAGAGGAGGATTCGAAGGTGGGAAGTATTGAGCTGCAGGACGTGAAATGCGA	466
Db	4311	CGGTGTGAGAGGAGGACTCAAGGTGGGAAGTATGAGCTTACAGGACGTGGAAATGGA	437
Qy	4697	GGAGAGCCCCCGGGAAGCGCTCAACTAAGGGTATTTAAATCTGAAGCAAGAGGCC	476
Db	4371	GGAGAGCCCGTGGGGAGGACGTCCAACTAGGGTATTTAAATCTGAAGCAAGAGGCC	443
Qy	4757	AAAAGATTGGAACCCCGCACCCCACTCTTTCAGAACTGTCTTGAAGAGAACTGTTGG	481
Db	4431	AAAGATTGGAAC-----GCCCGCGCCCACTCTTTCAGAACTGTGAAGAGAACTGTTGG	449
Qy	4817	AGTATGGAAGAAAGATCCCTGTCCAGGAGACAGGATTCATGTTACTGTAACGATTTGTA	486
Db	4490	AATTTATG-----GGAAGCAGATTCATGTTACTGTAACGATTTGTA	453
Qy	4877	TTATTTTGAATATTTCTATATAATTTTGAAGATGTACACATGTGTAATATAGAG	493

Db 4531 TTTATTKKGGGAATATTTCTATTAATATTTTARAGGTGTACACA - TGTATATATACATGG 4588  
QY 4937 GAAGATGTGAAGTGTATGATGTGGGCTTCTCCACTCTGCCCCAGAGTGTGAGACC 4996  
Db 4589 AATATGCTGACAGT -CTATTTCTTGGGGCTCTCCACTCTGCCCCAGAGTGTGAGACC 4647  
QY 4997 ACAGAGGAGCTCTCCGTTATTTGTGGGCTCCGTCACACCAACCAAGCTTATTAATG 5056  
Db 4648 ACA--GGGGCCCTTTCCTGCTGTATGCTGTCTGTGTCACACCAAGCTTAACTAG 4705  
QY 5057 CTMAA-----TTTCAGCATATGTTGCTGCTGCTTAATATTTGTAATTTACTTGT 5108  
Db 4706 TTTTAAAAAATCTCCAGCATATGCTGCTGCTGCTTAATATTTGTAATTTACTTGT 4765  
QY 5109 ATATTTCTATGCAATATTTGCTATGTAATGATTTATTTTGTAAAGTTTCTGTTAAA 5168  
Db 4766 ATATTTCTATGCAATATTTGCTATGTAATGATTTA-TTGTAAAGTTTCTGTTAAA 4824  
QY 5169 ATATTTAAATTTGCAATATTCACAACCTGTGTAATGTAATGTTACTGTTAACTTTCA 5228  
Db 4825 ATATTTAAATTTGCAATATTCACAACCTGTGTAATGTAATGTTACTGTTAACTTTG 4884  
QY 5229 AACACGCTATGCTGATTAATTTTGTTTTAATGACGAGATATGAAGAAGC 5280  
Db 4885 AACACGCTATGCTGTA--TTGTTTAAAGACGACGACATGAAGAAGC 4931

RESULT 8  
PCT-US95-13233-3  
; Sequence 3, Application PC/TUS9513233  
; GENERAL INFORMATION:  
; APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY  
; TITLE OF INVENTION: Patched Genes and their use  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert  
; STREET: Four Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/13233  
; FILING DATE: 06-Oct-1990  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Rowland, Bertam I  
; REGISTRATION NUMBER: 20015  
; REFERENCE/DOCKET NUMBER: A60190-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-781-1989  
; TELEFAX: 415-398-3249  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5187 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; PCT-US95-13233-3

Query Match 71.9%; Score 3801.2; DB 4; Length 5187;  
Best Local Similarity 88.1%; Pred. No. 0;  
Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

QY 446 CGGTGCCCCGGGAGCGCCGCTGAGCGCGGAGCGGACGAGCGAGGGGGGCTGCGCCG 505  
111 1111 111 111 111 1111111111111111 1111 1 11 111

Db 120 CGGGCCCTGCGGACGAGCGCCGCGGAGGCGGACAGCGACCGGGGACCGCACC 179  
QY 506 TGTGCGCGCGCGGACCGGACATATCTGCACCGGCCACTACTGCGAGCGCCCTTCG 565  
Db 180 C---GCCGGCGGACCGGACATATCTGCACCGGCCACTACTGCGAGCGCCCTTCG 236  
QY 566 TGTGAGCAGATTTTCAAGGGGAGGCTACTGCGCGAAGCGCCACTGTGCTGAGAGC 625  
Db 237 TGTGAGCAGATTTTCAAGGGGAGGCTACTGCGCGAAGCGCCACTGTGCTGAGAGC 296  
QY 626 GAGTTTCAAGACTTTTAACTGGGTGTTTCAATTCAAAATACTGGGGCAAGTT 685  
Db 297 GAGTTTCAAGACTTTTAACTGGGTGTTTCAATTCAAAATACTGGGGCAAGTT 336  
QY 686 CTGGTTGGGCTCTCTATTTTGGGCTTTCGCGGTGGATTTAAAGCAGCAAGCT 745  
Db 357 TTTGGTTGGGCTCTCTATTTTGGGCTTTCGCGGTGGATTTAAAGCAGCAAGCT 416  
QY 746 CGAGACCAAGCTGAGAGAGCTGTGGTGAAGTTGAGAGCAGTAACTGTAATTTAA 805  
Db 417 CGAGACCAAGCTGAGAGAGCTGTGGTGAAGTTGAGAGCAGTAACTGTAATTTAA 476  
QY 806 TTAATCTGCGGAGGATTTGAGAGAGGCTATGTTAATCTCACTCATGATACAGAC 865  
Db 477 TTAATCTGCGGAGGATTTGAGAGAGGCTATGTTAATCTCACTCATGATACAGAC 536  
QY 866 CCTTAAAGAGAGGATGCTAATGCTCTGACACAGAGCGCTCTACACACCTGAGCTC 925  
Db 537 TCCAAAGAGAGAGGCGCTAATGCTCTGACACAGAGCGCTCTCTGACACCTGAGCTC 596  
QY 926 GCGACTCCAGCGGACCGCTGTCCATGTATACATGTATACACAGCAGAGGCAATTTGACA 985  
Db 597 AACACCTCCAGCGGACGCTGTGACAGCTTACATGATTAACAGCAATGAGAGTTGAGACA 656  
QY 986 TTTGTGTCAAAATTCAGAGAGCTTATACAGAGAGAGGTTTAACTGATGATTAATAGA 1045  
Db 657 TTTGTGTCAAAATTCAGAGAGCTTATACAGAGAGAGGTTTAACTGATGATTAATAGA 716  
QY 1046 ATATCTTACCTTGTGTTGTTATTAATACCTTTGAGACTGCTTGGAGAGCGGCAATT 1105  
Db 717 ATACCTTACCTTGTGTTGTTATTAATACCTTTGAGACTGCTTGGAGAGCGGCAATT 776  
QY 1106 ACAGTGTGGAGACGATCTCTAGTAAACCTCTTGGGAGGCAAACTCGACCC 1165  
Db 777 ACAGTGTGGAGACGATCTCTAGTAAACCTCTTGGGAGGCAAACTTTGACCC 836  
QY 1166 TTTGGAATTCCTGAGAGAGTTTAAAGAAATTAATCAATCAAGTGGAGACAGTGGAGAAAT 1225  
Db 837 CTTGGAATTCCTGAGAGAGTTTAAAGAAATTAATCAATCAAGTGGAGACAGTGGAGAAAT 896  
QY 1226 GCTGAATTAAGGCTGAGGTTGCTATGTAATGAGACCGCCCTGCTCAATCCGCCGA 1285  
Db 897 GCTGAATTAAGGCTGAGGTTGCTATGTAATGAGACCGCCCTGCTCAATCCGCCGA 956  
QY 1286 TCCAGACTGCGCCCGCACACCGCCCAAAATTTCAACCAACCTCTGATATGGCCCT 1345  
Db 957 CCCAGATGCGCCCGCACACCGCCCAAAATTTCAACCAACCTCTGATATGGCCCT 1016  
QY 1346 TGTTTGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1405  
Db 1017 TGTTTGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076  
QY 1406 GATTGTGGGTGGACAGTCAAGAACAGCACTGGAATCTGTCAGCGCCCTGCTGCA 1465  
Db 1077 GATTGTGGGTGGGTACCGTCAAGAAATGCGATGGAATCTGTCAGCGCCCTGCTGCA 1136  
QY 1466 GACCATGTTCCAGTTATTAATGATCCCAAGCAAAATGATAGAGACTTCAAGGGGTGCGGTA 1525  
Db 1137 AACCATGTTCCAGTTATTAATGATCCCAAGCAAAATGATAGAGACTTCAAGGGGTGCGGTA 1196  
QY 1526 TGTCTCACATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1585  
Db 1197 TGTCTCACATCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1256



OY 1586 GACATATGTGAGTGGTTCATCAGAGTGTGCACAGACTCCACTCAAAAGTCTTTC 1645  
DB 1257 GACTTACGTGGAGGTGGTTTATCATAAAGTGTGCCCCCAAACTCCACTCAAAAGTCTTTC 1316  
OY 1646 CTTCACACACACGACCTGTGACAGACATCTGAAATCCCTTCTGTGACGTCACTGTCTCG 1705  
DB 1317 CTTCACAAACACACACCTGTGACAGACATCTGAAATCCCTTCTGTGATGTCACTGTCTCG 1376  
OY 1706 CGTGGCAGGCGCTACTTACTCATGCTGCGCTATGCTGTCTAACCATGTCTGCGTGGGA 1765  
DB 1377 AGTGGCAGGCGCTACTTACTCATGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGGA 1436  
OY 1766 CTGCTCCAAAGTCCAGAGGTCCGTTGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1825  
DB 1437 CTGCTCCAAAGTCCAGAGGTCCGTTGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1496  
OY 1826 GGTGAGAGAGCTGGGCTGTGCTCATGATGCGAATTCCTTTAAGCTGTGCAACACTCA 1885  
DB 1497 GGTGAGAGAGAGCTGGGCTGTGCTCATGATGCGAATTCCTTTAAGCTGTGCAACACTCA 1556  
OY 1886 GGTGAGAGAGAGCTGGGCTGTGCTCATGATGCGAATTCCTTTAAGCTGTGCAACACTCA 1945  
DB 1557 GGTGAGAGAGAGCTGGGCTGTGCTCATGATGCGAATTCCTTTAAGCTGTGCAACACTCA 1616  
OY 1946 CTTCAGTGAAGAGACACAAATTAAGAAATCCCTTTTGAAGACAGACCGGGAGTGCCT 2005  
DB 1617 ATTCACTGAAGACAGACAAATTAAGAAATTCCTTTTGAAGACAGACCGGGAGTGCCT 1676  
OY 2006 GAAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2065  
DB 1677 CAAGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736  
OY 2066 GGGCGGCTTAATCCCAATTCCTGCTGTGCGGGCTTCTCCCTCCAGAGAGAGAGAGAGAGAG 2125  
DB 1737 GGGCGGCTTAATCCCAATTCCTGCTGTGCGGGCTTCTCCCTCCAGAGAGAGAGAGAGAGAG 1796  
OY 2126 GGTGCTCAATTTTGGCATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 2185  
DB 1797 GGTGCTCAATTTTGGCATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 1856  
OY 2186 TCGACGCGAGAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2245  
DB 1857 CAGAGCGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916  
OY 2246 AGTATTCAGGTGTGACCTGAGGCTTACACGACACACGACAAATACCGGCTTACAGGCC 2305  
DB 1917 GGTATTCAGGTGTGAGCCACAGGCTTACACAGAGAGCTTACAGAGAGAGAGAGAGAGAG 1976  
OY 2306 CCCACCTCCCTACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2365  
DB 1977 CCCACCTCCCTACAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2036  
OY 2366 TGTCCAGCTCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2425  
DB 2037 GGTCCAGCTCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2096  
OY 2426 GCGCTCCGAGATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2485  
DB 2097 AGCTCTGAGATCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2156  
OY 2486 CCCAGAGAGACACAGCTTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2545  
DB 2157 TCCCGAGAGACACAGCTTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2216  
OY 2546 CTGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2605  
DB 2217 CTGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2276  
OY 2606 TCGCTTCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2665  
DB 2277 TCGCTTCTCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2336

OY 2666 GGGGCTCAGCCTTTATGTGACACACCGAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2725  
DB 2337 GGGGCTCAGCCTTTATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2396  
OY 2726 ACTCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2785  
DB 2397 TCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2456  
OY 2786 CAACATGTATATATGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2845  
DB 2457 CAACATGTATATATGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2516  
OY 2846 CCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2905  
DB 2517 CCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2576  
OY 2906 CAAATGTGTGCTGCTACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2965  
DB 2577 CCAATGTGTGCTGCTACTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2636  
OY 2966 TGACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3025  
DB 2637 TGACTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2696  
OY 3026 CCTTGGCTTACAAAGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3085  
DB 2697 CCTTGGCTTACAAAGCTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2756  
OY 3086 GTTGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3145  
DB 2757 GTTGCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2816  
OY 3146 CTACCTGAGGCTTGTGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3205  
DB 2817 CTACCTGAGGCTTGTGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2876  
OY 3206 CCGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3265  
DB 2877 CCGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2936  
OY 3266 GAGATTCGCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3325  
DB 2937 GAGATTCGCGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2996  
OY 3326 GCGGAGACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3385  
DB 2997 ACAGAGACCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3056  
OY 3386 TACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3445  
DB 3057 TACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3116  
OY 3446 CATGCGCTCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3505  
DB 3117 CATGCGCTCCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3176  
OY 3506 CGTGTGCGGTGTCTCTCTTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3565  
DB 3177 AGTGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3236  
OY 3566 GCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3625  
DB 3237 TCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3296  
OY 3626 GCGCGGTGATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3685  
DB 3297 GCGCGGTGATCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3356  
OY 3686 TTTGGCTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3745  
DB 3357 TTTGGCTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3416  
OY 3746 CATGTTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3805





QY	2606	TCCTTTCCCTTTGAACCAAAAGCCAGGTAGTGTGATCTTTCCTTTTCTTGTGGCTTGTCT	2605
Db	2277	TCCTTTCCCTCTGAAACCCCAAGCCAGAGTGTGTGTAATCTTCTTTCTGTGGGCTTGTCT	2336
QY	2666	GGGGGTGAGCCTTTATGTGCACACACCAGGTGAGACAGGGGTGAGACTTACAGCAATGT	2725
Db	2337	GGGGGTGAGCCTTTATGTGGACACCCGAGTGAAGACGGGCTGGACCTTCACGCAATGT	2396
QY	2726	ACCTGGGGAACACAGAAATATGACTTTATGTGCTGCACAAATTCAAATACCTTTCTTCTA	2785
Db	2397	TCCCGGGGAACCAAGATAATATGACTTCATAGCTGCCAGTTCAAGTACTTCTCTTCTA	2456
QY	2786	CACACTGTATATAGTCACCCAGAAAGCAGACATCCGGAATATCCAGACTTACTTTACGA	2845
Db	2457	CACACTGTATATAGTCACCCAGAAAGCAGACTACCCGATATTCAGACACTTACTTACGA	2516
QY	2846	CCTACACAGAGATTTACAGTAACGTAAAGTATGTCAATGTTGGAAGAAAACAAACAGCTTC	2905
Db	2517	CCTTATATAAGATTTACAGAAATGTGAATATGTCAATGCTGTGAGAGAAACAAACACTTTC	2576
QY	2906	CAAAATGTGCTGCACACTTACAGAGCTGGCTTCAGGACCTTCAGAGATGCATTTGACAG	2965
Db	2577	CCAAATGTGCTGCACACTTACATTGAGAGCTGGCTTCAGGACCTTCAGAGATGCATTTGACAG	2636
QY	2966	TGACGTGGGAAACCGGGAAATATATCACCAAACAAATTAACAAGATGATTCAGACATGGAGT	3025
Db	2637	TGACGTGGGAAACGTGGAGGATCATGCGCAAAACATTTAAAAATGATCAGATGACGGGT	2696
QY	3026	CCTTGCTTACAAACTCTCTGGTGCAAAACGGGACGGCGATTAAGCCATAGCAATCAGCA	3085
Db	2697	CTCTCCCTTACAAACCTCTGGTGCAAGCTGGACCTGGACCGAGCAAGCCCATGACATTAAGTCA	2756
QY	3086	GTTGACTAAACAGCGCTGTGGATGCAATGGCAATTAATCCCAAGGCTTTCTTACAT	3145
Db	2757	GTTGACTAAACAGCGCTGTGGATGAGCCAGCATTAATCCGAGGCTTTCTTACAT	2816
QY	3146	CTACCTGACGGCTTGGGTTAGCAGACGCCCTGCGGTATGCTGTGCTCCAGGCCCAACAT	3205
Db	2817	CTACCTGACCGCTTGGGTTAGCAGCAACACCCTGTAGTTTACGGTCCCTCCAGGCCCAACAT	2876
QY	3206	CGGGCCACACCGACCGAATGGGTTCCACGACAAAGCCGATACATGCTCTGAACAGAGCT	3265
Db	2877	CGGGCTTACACCGGCGGAGTGGSTCCATGACAAAGCCGATACATGCGACAGACAGGCT	2936
QY	3266	GAGAAATCCGGGACGAGAGCCCATGAGTATGCCCAGTTCTTACTTACACAGGTT	3325
Db	2937	GAGAAATCCGAGCGAGAGGCCCATGAGTATGCGTCAAGTTCTTCTTACTTACACAGGCTT	2996
QY	3326	GGGGGACACCTTCAGACTTTGTGGAGGCATTAAGAAAAGTAAGAACCATCTGCGACACACTA	3385
Db	2997	ACGAGACACCTTCAGACTTTGTGGAGGCATTAAGAAAAGTAAGAGTATCTGTAAACAACTA	3056
QY	3386	TACGACCTTGGGGCTGTCCAGTTACCCCAACGGGCTACCCCTTCTCTTGTGGAGCAGTA	3445
Db	3057	TACGAGGCTGGGACTGTCCAGCTACCCCAATGGCTACCCCTCTGTGTTGGGAGCAATA	3116
QY	3446	CATCGGCTTCCGCGCACTGGTGTGCTGTCTCATCAGAGTGGTGTGGCCGCGACATTCCT	3505
Db	3117	CATCAGGCTTCCGCGCACTGGTGTGCTATCATCAGAGTGGTGTGGCCGCGACATTCCT	3176
QY	3506	CGTGTGGCGCTGTCTTCCCTTGTGAACCCCTGAGCGCGCGGAGTCAATTTGATGTGCTGGC	3565
Db	3177	AGTGTGGGCAGTCTCTCTCTGAACCCCTGGAGCGCGGGATCTATGTGCTGGCTGGC	3236
QY	3566	GCTGATGACGGTGAAGCTGTTCCGATGATGATGGGCTTATGGGAATCAAGCTCATGTGCCCT	3625
Db	3237	TCTGATGACCGGTTGAGCTCTTTGGCAATGATGGGCTTATTTGGGATCAAGCTGAGTGTGCT	3296
QY	3626	GGCCGTGGTATATCTGATTCGCTTCTGTTGGATATGAGAGTGGAGTTCAACCGTTCAGCTTGC	3685
Db	3297	GCCCTGTGTATCTCTGATTCGATCTCTGTTGGCATGTGGAGTGGAGTTCAACCGTTCAGCTG	3356
QY	3686	TTTGGCCCTTTCAGACGGCATGCGCGACAAAGACCGAGGGCTGTGCTTGCCTTGGAGACA	3745

Db	3357	TTTGGCCCTTTCGACAGCATTGGGGACAAAGAACCAAGGGGCTATGCTCGCTTGGACAA	3416
Qy	3746	CATGTTTGCACCCGTCCTGGATGGCGCGGTGTCCACTGTGCTGGGAATGCTGATTCCTGGC	3805
Db	3417	CATGTTTGCCTCCGCTTCGGAGGGGTGCTGTCCACTGTGCTGGGTGTACTGATTCCTTGC	3476
Qy	3806	GGGATCTGAGTTTGCAGTTTCATTTGTAGGTAATTTCTTGTCTGTGCTGGGATCTCCACCAT	3865
Db	3477	AGGGTCCGAAATTTGATTTTCATTGTTCAGATACACTTCTTGGCGTCCGGCATTTCCACCGT	3536
Qy	3866	CCTGCGCGCTTTCGAATGGCGCTGGTTTTGTCTCCGCTGTTTTGTCTTTTCTTTGGACATA	3925
Db	3537	CTTGGGGGGTTCGAATGGACTGTGTTCTGTGTCTGTCTCTCTCTTATCTTTTGGACCGG	3596
Qy	3926	TCCCTAGGTGTGTCCAGCCCAACGGGTGTGAACCGCTGGCCACACCTCCCTCCGAGCCACC	3985
Db	3597	TCCCTAGGGGTGTCCAGCCCAATGGCTTAACCGACTGCCACTCCTTCCTGGCCGTGAGCGCGC	3656
Qy	3986	CCCCAGCGTGTTCGCCCTTTCGCCATGCGCGCCGGCCACACGCAACAGCGGTCTTGATTTCTTC	4045
Db	3657	TCCAGATGTGCTCCGGTTTCCGCTGCGCTCTGTGTCAACGAACATGGGTCTGATTTCTTC	3716
Qy	4046	CGACTTCGAGTATAGTTCCACAGCAAGTATGTACAGGCTTCACAGAGACTTCGGCAGTA	4105
Db	3717	CGACTTCGAGTACAGTCTTCAGACACGGGTGTGTGGCATCAGTAGAGACTCAGGCATA	3776
Qy	4106	CGAGCGCCAGCAGGGGCGGGGAGGCCCTGCCACCAAGTATGTGGAAAGCCACAGAAAA	4165
Db	3777	CGAAGCACAGCAGGGGTGCCGGAAGCCCTGCCACCAAGTATGTGGAAAGCCACAGAAAA	3836
Qy	4166	CCCCGTCCTTCCGCACTCCACGTGTGTGTCCATCCGAAATCCAGGATCACCCACCCCTCGAA	4225
Db	3837	CCCTGTCTTGGCCGGTCCACGTGTGTCCATCCGGACTCCAGACATCAGCTTCCCTTGAC	3896
Qy	4226	CCCCAGACAGCAGCCCCACTGTGACTCAGGGTCCCTGCTCCGAGCGGCAAGCCACGA	4285
Db	3897	CCCTGGCAACAGCCCCACTGTGACTCTGTGCTCTTGTCCCTCGAGCGCAAGCCACGA	3956
Qy	4286	GCCCCGAGGAGACCCCCCAGANAAGGCTGTGTGCCACCCCTGTACAGACCGGGAGAGA	4345
Db	3957	GCTTCGAAGGATCCCCCTTAGAAGAGGCTTGGCGGCAACCCCTTACAGACCGCGCAGAGA	4016
Qy	4346	CGCTTTTGAATTTCTACTGAAGGAGATTCTGTGCCCTAGCAATAAGGAGCCCGCTGGGGGCC	4405
Db	4017	CGCTTTTGAATTTCTACTGAAGGAGATTCTGTGCCCTAGCAATAAGGAGCGCTCAGGGCC	4076
Qy	4406	TGCGGGGGCCGTTTTCACAACTCTGGAAACCAAGCTCCACTTGCATTTGGCGAGCTCCGT	4465
Db	4077	CCGTGGGGCCCGTTTTCACAACTCTGGAAACCAACTCCACGCGCATTTGGCGAGCTCTGT	4136
Qy	4466	GCCCGGTACTGCGAGGCCATCAACACTTGTAGCGGCTTGTGCCCTGTGACTGTGCGCGT	4525
Db	4137	GCCCGGTACTGCGAGGCCATCAACACTTGTAGCGGCTTGTGCCCTGTGACTGTGCTGT	4196
Qy	4526	GCAACCGACCGCTGTCCCTGGGCTGGGCGGAACCCCGAGGGGAGCTTTCGCCAG- ---	4581
Db	4197	GCATCCCCCG- ---CCTGAGACTGTGGGCCCAACCCCGAGGGGGGCGCTGTCCAGGCTA	4250
Qy	4582	-----GCTACCCGTAGACTACACAGCGCGCTTTTGAAGAGCCCCACGCTTGTCCAGT	4636
Db	4251	TGAGAGCTTACCTGTAGACTGTATCGGGGGTATTTTGAAGGATTCCTCATGTGCTTTTCAATGT	4310
Qy	4637	CCGCTGTGAGAGGAGGATTTCGAAGGTGGAAGTCAATTGAGCTGCAGAGAGTGAATCGA	4696
Db	4311	CAGGTGTGAGAGGAGGAGCTCAAGGTGTGAGAGTCAATAGAGCTGTGAATGTGA	4370
Qy	4697	GGAGAGCCCCGGGGAAGCAGCTCCAACCTAGAGGTATTTAAATCTGAACCAAGAGAGCC	4756
Db	4371	GGAGAGCCCCGGGGAAGCAGCTCCAACCTAGAGGTATTTAAATCTGAAGCAAGAGAGCC	4430
Qy	4757	AAAGATTGGAAGCCCCCACCCTCTTTCAGAACTGTCTTGAAGAGAACTGATTGG	4816

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Db 4431 AAGATTGGAAA-GCCCCGCCCCACCTCTTCCAGAACTGCTTGAAGAACTGCTTGG 4489
Oy 4817 AGTTATGAAAAAGATGCCCTGTGCCAGACACAGCTTATGTTACTGTAAACCGATGTA 4876
Db 4490 AATTATG-----GGAGGACAGTTCATTTGTACTGTAACTGATTTGTA 4530
Oy 4877 TTATTTTGTAAATATTTCTAATAATATTTAAAGATGTACACATGTGTAAATATGAAAG 4936
Db 4531 TTATTTKGTGAATATTTCTAATAATATTTAAAGATGTACACA--TGTAAATATACATGG 4588
Oy 4937 GAAGGATGTAAGTGTATGATCTGGGCTTCCACCTCCGCCAGAGTGGAGGCC 4996
Db 4589 AATATGCTGATAGT-CATTTTCCTGGGCTCTCCACTCTCCCGGAGGTGGAGACC 4647
Oy 4997 ACAGTGGGCTCTCCGATATTTGTGCAATGGGCTCCGCCAACCAAGCTTCATTAGT 5056
Db 4648 ACA--GGGGCCCTTCCCTGTGTACATTTGCTGTGCCAACCAAGCTTAACTTAG 4705
Oy 5057 CTTAAA-----TTTACGATATGTTGCTGCTGCTTAAATATTTATATTTACTTGT 5108
Db 4706 TTTTAAAAAATCTCCAGCATATGCTGCTGCTTAAATATTTACTTGT 4765
Oy 5109 ATATTTCTATGCAAAATATTTGCTATGTAATAGATTTATTTGTAAGGTTTCTGTTAAA 5168
Db 4766 ATATTTCTATGCAAAATATTTGCTATGTAATAGATTA--TTTAAAGGTTTCTGTTAAA 4824
Oy 5169 ATATTTTAAATTTGCAATATCAACACCTGTGTAGTATGAAATGTTACTGTTAACTTTCA 5228
Db 4825 ATATTTTAAATTTGCAATATCAACACCTGTGTAGTATGAAATGTTACTGTTAACTTTTG 4884
Oy 5229 AACACGATATGCGATATATTTTGTATGAGCATATGAAAGAAC 5280
Db 4885 AACACGATATGCGATATATTTTGTATGAGCATATGAAAGAAC 4931

RESULT 10
US-08-356-060A-42
: Sequence 42, Application US/08356060A
: Patent No. 5844079
: GENERAL INFORMATION:
: APPLICANT: Ingham, Phillip W.
: APPLICANT: McMahon, Andrew P.
: APPLICANT: Tablin, Clifford J.
: TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing
: TITLE OF INVENTION: Proteins and Uses Related Thereto
: NUMBER OF SEQUENCES: 47
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: LAHIVE & COCKFIELD
: STREET: 60 State Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII(text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/356,060A
: FILING DATE: 14-DEC-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/176,427
: FILING DATE: 30-DEC-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Vincent, Matthew P.
: REGISTRATION NUMBER: 36,709
: REFERENCE/DOCKET NUMBER: HMT-006CP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 227-7400
: TELEFAX: (617) 227-5941
: INFORMATION FOR SEQ ID NO: 42:

```

```

: SEQUENCE CHARACTERISTICS:
: LENGTH: 3900 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..3897
: US-08-356-060A-42

Query Match 7.8%; Score 411.8; DB 2; Length 3900;
Best Local Similarity 48.9%; Pred. No. 2,7e-89;
Matches 1730; Conservative 0; Mismatches 1542; Indels 263; Gaps 13;

Oy 537 CGGCCAGTACTGCGAGCCCGGCTTGTGCTGAGACATTTCCAAAGGGGAAGGCTACT 596
Db 82 CGCACAGCTGGGTGAGCCGCCAAGTGGCGCTGATCAGATAGATAAGGCGAAGCGCGT 141
Oy 597 GGGCGAAGAGCCGCACTGTTGGGAGAGGCAAGTTTTCAGAGACTCTTATTTAACTGGGT 656
Db 142 GGCAGCCGCGCGCGCATCTATCTGCGATCAGTATTCAGTCCACCTCGAAGCCCTGGC 201
Oy 657 TGTTCATTTCAAAAAAATCTGCGCAAGTTCTTGTGTTGGGCTCTCATATTTGGGGCC 716
Db 202 AGCTTCGTCGCAAAAGACAGCCGGGCAAGTGTCTATTTGCTGCTATCTGTTCTAGCAC 261
Oy 717 TTCGCGTGGGATTTAAAGCAGCAACCTCGAGACCAACCTGAGAGAGCTGTGGTGGAA 776
Db 262 TTCGCGTGGGCTTAAAGAGCGCCGAGATCCACTCCAAAGGTGCACAGCTGTGATCAG 321
Oy 777 GTTGAGAGACGAGTAAAGTGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 836
Db 322 GAGGCGCGCGGCTGAGGCGGAGTGGCTTACACACAGAGATGCGGAGAGAG 381
Oy 837 ATGTTAATCTCAACTCATGATATACAGACCCCTTAAGAAAGAGTGTAAATGTCGTGAC 896
Db 382 TCGGCCAGCATACGCTGCTCATTTTCAGAGACCCAGACCCGCAAGCGCTCGCTCAT 441
Oy 897 ACAGAAAGGCTCTTACAAACCTGAGCTGGGCTCGAGCCAGCCCTGTTCATATATAC 956
Db 442 CCGCGGCGCTCTTCCACCTGAGGCTGCTGCTGTAAGGCGCACCGCGCTCAAGGTGCAC 501
Oy 957 ATGTACAACAGCACTGTAATTTGGAACAATTTGTTTAAATATCAGAGAGAGC---TTATC 1013
Db 502 CTCTACGACACCGAATGGGGGCTGGCGGACATGTGCAACATGCGGACAGCCCTCTTCC 561
Oy 1014 ACAGAAACAGGTTACATGATGATATATATATATATATATATATATATATATATATAT 1073
Db 562 GAGGCGATCTACTACATGAGACAGATCTGCGCACCTCATATTCGCTGATATATACAG 621
Oy 1074 CCTTGGACCTGTTCTGGGAAGGGCGGAATTAACAGTCTGGGACAGCATATCTCT--- 1129
Db 622 CCGCTGGACCTGTTCTGGGAAGGGCGGAAGCTGTTGGGTCGGAATTAACAGGCTGTTATA 681
Oy 1130 -----AGGTAAACCTCTTGGGCTGGAACAATTTGACCTTTGGAATTCGGAAGAG 1184
Db 682 CCAGGCTCAACCAACAGACTCTGTGAGACACATGAATTCGCTCTGTGATGACATAT 741
Oy 1185 TTTAAG-----AAATTAATCATCAAGTGAGAGCTGGAGGAATG 1226
Db 742 ATGAAGCAGAGAGATGTCCGAGGAAAAAGATCACCTTGACTGTGAGACCGTGGAGATAC 801
Oy 1227 CTGAATTAAGGCTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1286
Db 802 ATGAAGGCTGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 861
Oy 1287 CCAGACTGCCCGCCAGCCAGCCCAACCAAAATTTCAACCAAACTGTTATGAGCCCTT 1346
Db 862 CCCAATTTGCCGAGACAGGACCGCAAAAGAAAGACAGACCCAGCCGCGGATGTGGAGGC 921
Oy 1347 GTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1406

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Db 922 ATCTGTCCGAGGCTGTAGGTTATGCGGAGACATCTGCGGAGAGGCTG 981  
QY 1407 ATTGTGGTGGCAGACAGTACAGACAGCACTGGAATCTGTCAGCGCCATCCCTGCAG 1466  
Db 982 ATTGTGGGCGGAGGAGAGAGACCGGACGACCTTGAGAGAAAGCCGAGCCGCTGCGAG 1041  
QY 1467 ACCATGTTCCAGTATATGACCTCCCAAGCAATGTACGAGCACTTGAAGGGGTACAGAT 1526  
Db 1042 TCGGTGTGTCAGCTGATGATACCGAGAGAAATGTACGACCAATGGCAGACAACTACAG 1101  
QY 1527 GTCTCACACATCAACGTGAGAGAGACAAAGCGCAGCCATCCCTGAGGCTGCGAGAG 1586  
Db 1102 GTGACACATCTTGGATGAGACGAGAGAGAGAGGAGGTGTTGAAACCTGCGGAGCGC 1161  
QY 1587 ACATATGTGGAGGTGTCTCATCAGAGTGTCCGACAGAA-----CTCCACTCAA 1634  
Db 1162 AACCTTTCCGCGGAGGTGGAACAGCTGCTAGCTAAACAGTCAGAAATGGCCACCACTAC 1221  
QY 1635 AAGGTGCTTCTCTCACACACGACCTGGACGACATCCGAAATCCTTCTGTGACGTG 1694  
Db 1222 GATATCTACGTTTCACTGCTGCGCTGCTACGATGACATCTGCGCAAGTTCTCCATCCG 1281  
QY 1695 AGTGTCAATCCGCTGCGCAGCGGCTACTACTCATGCTGCGCTATGCTGTCAACATG 1754  
Db 1282 AGCGCTTGTCCATGTTGATGAGGCTGCGGCTGACCGCTTTGTATGCTTGCACGCTG 1341  
QY 1755 CTGGGCT---GGGACTGCTCCAGTCCAGAGTGGCGGCTGGCGGCTGGCGCTGCG 1811  
Db 1342 CTGCGCTGAGAGGACCGGCTGCTGAGACAGAGTGTGCGGCTGGCGGAGTTCGCTG 1401  
QY 1812 GTTCACATGTAGTGTGTCAGAGAGTGGGCTGCTCATGATGAGAAATTCCTTTAAC 1871  
Db 1402 ATGTGCTTTAGTAACCGCGCGGATTTGGGATTTGACGCCCTGCTGCTGATTCGTTTCAAT 1461  
QY 1872 GCTGACACACTGAGTTTGGCAATTTCTGCTTGTGTTGTTGTTGATGATGTTT 1931  
Db 1462 GCGCGACACACCGAGGTGTTCCGTTTGGCTGTGCTGGGCTGCATCATCTTC 1521  
QY 1932 CTTCGCGCCACGCGCTTCAAGTGAACAGAGCAAGTAATAAGAAATCCCTTTGACAGAG 1991  
Db 1522 ATGTGACCGGCTGCTATGCGGAGAGCAATCGGCG-----GGAGCAG 1563  
QY 1992 ACCGGGAGTGTGCTGAGAGCAGAGAGGACGTCGCTGACGTCATCAGCAATGTC 2051  
Db 1564 ACCAAGCTGATTTCTCAAAAGTGGAGCGAGCATCTGTTGAGTCTGACACCGCA 1623  
QY 2052 ACAGCTTCTTATGCGCGCTTAATCCCAATTTCCGCTGTCGCGGCTTCTCCCTCAG 2111  
Db 1624 GGATCTTCTTGGCGCGCTTTATTCGCGTGGCGCTTTGAAGGTATTCGTGTCAG 1683  
QY 2112 GCAGCGTGTAGTGTGCTTCAATTTTGGCATGTTGCTGCTCATTTTCTTCAATTC 2171  
Db 1684 GCTGCACTGTAATGTGCTCCAAATTTGCGAGGCTCTATTTGTTTTTCCGCGCATGAT 1743  
QY 2172 AGCATGATTTATTCAGAGCAGAGAGAGAGAGATGATATTTTCTGCTGTTTACAGC 2231  
Db 1744 TCGTTGATCTTCAAGAGATACCGCGGAGGAGGAGCATCTTCTGCTGCTGTTTCCG 1803  
QY 2232 CCTGCGCTGAGAGATGATTTAGGTTGAATCTCAGGCTTACCGCAGACACAGCAAT 2291  
Db 1804 GTGTGGAAGGAACAGCGGAGGTGACACCGGTGCTGCGCTGAACAACAACAGGG 1863  
QY 2292 ACCCGCTACAGCGCCCACTCTCTACAGACAGCAGCTTTGCCATGAAAGCAGAT 2351  
Db 1864 GCGGGGCGCGGATCCGAAAGGTGACACACACACAGAGGTGGCGCTGCCCGCCAGAT 1923  
QY 2352 ACCATGACATGCTGCTCCAGCTCCGACGAGTACGACCCCAACAGCAGTGTACTAC 2411  
Db 1924 CCTGTGCTG-----1932  
QY 2412 ACCACCGGTAGCGCGCTCCAGATCTCTGTGACGCGCTACCGTGAACAGAGAC 2471

Db 1933 -----GACAGAGGCGCAGCATCTGCG-----1956  
QY 2472 CTCAGCTGCCAGAGCCAGAGAGACAGCTCCCAAGGAGCCTGCTCTCCAGTTCTCC 2531  
Db 1957 -----1956  
QY 2532 GACTCCAGCTCCAGCTGCTCGAGCCCGCTGTACGAAGTGAAGTCACTCTCTTTGCT 2591  
Db 1957 -----AGCAGTCACTCACTGCGGCTCTCTG-----CTGCGCAACATTCGCC 1998  
QY 2592 GAGAGCAGTATGCTCTTCTCTTCTTAACCAACCAAGCAAGTATGATGATCTTCT 2651  
Db 1999 TTTGAGCAGTACCTCTCTCTCTATGCGAGCTGGGTGAAGTCTGACCGTTATGGT 2058  
QY 2652 TTTCTGCGGCTTGGGCGGCTTATGCGACCAACCGGAGTGAAGAGCGGCTGAGC 2711  
Db 2059 TTTCTGCGGCTTCTATATCAGCTTGTATGCTTCCACGCGCTTCAAGATGGCTGAC 2118  
QY 2712 CTACGAGCATTTTACCTCGGGAACAGAGATATGACTTATTTGTCACAAATTCAA 2771  
Db 2119 ATTATGATCTGCTGCCAGAGCAGACAGAGCAAGATTTCTGATGCTCAAACTCGG 2178  
QY 2772 TACTTTTCTTCTACAACTATATATAGTACCCAG---AAGCAGACTACCCGATATC 2828  
Db 2179 CTCTTGGCTTACACAGATATGCGTTACCGAGGCACTTGAATATCCACCGAG 2238  
QY 2829 CAGCAGTACTTACAGACTACAGAGATTTACGTAACGTGAAGTATGATGTTGAA 2888  
Db 2239 CAGCAGTGTGCTCAGAGCACTACATGATTTCTTTGCGCGGTGCCACATGATCAAGAT 2298  
QY 2889 GAAACAAACAGCTTCCCAAAATGTGCTGCTACTTACAGACTGCTTCAAGGACT 2948  
Db 2299 GATATGATGAGACTGCGGAGCTTCTGCTGCTTCTGCTCAGAGTGGCTGATATCTG 2358  
QY 2949 CAGGATGCTTTGACAGTACT---GGGAAACCGGGAATATCAGTCAAAATATACAG 3005  
Db 2359 CAANAATATTCAGAGAGATACCGGAGGAGGCTGACCAAGAGATGCTGTTCCCA 2418  
QY 3006 AATGATCAGAGATGAGATGCTTGCCTACAACTCTGTTGCAACCGGAGCGGCTAT 3065  
Db 2419 AAGCGCAGAGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2478  
QY 3066 AAGCGCATTCAGATCAGCAGTAAAGAGTCTGCTGAGTATGAGATGCTATCT 3125  
Db 2479 AACCCGCTGCAAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2538  
QY 3126 AATCCAGGCTTCTATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3185  
Db 2539 AACCAAGCGGCTTCTATCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2597  
QY 3186 GCTGCTCCAGGCGCAACATCCGCGCAGCAGCAGCAGATGAGT-----3230  
Db 2598 GGAGCTTCTGCGGCAATTTGATCCGGAACCGCGCAGCAGCTTCTGAGCGCAAT 2657  
QY 3231 -----CAGCAGAAAGCGCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3277  
Db 2658 GTATCCGGAACCGCGCAGATTTTTCACCAACCAAGAGTACGATCTTAAGATCCCA 2717  
QY 3278 AGCAGAGCCCAATCAGATGAGTCCCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3337  
Db 2718 GAGTCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2777  
QY 3338 AGACTTGTGAGGCAATTTGAAAGATGAGGCACTGACAGCAATATACGAGCTGAG 3397  
Db 2778 GCAATCAAGACCCCTGATGATGCTATTTTCCGAGCTGAGGCTGAGGCTGAGGCTGAG 2837  
QY 3398 GCTGTCCAGTTATCCCAAGGCTTACCTTCTTCTGAGGAGGCTATGAGGCTGAG 3457  
Db 2838 CTTGCGCAATATCAGTCCGCTATTTCTTCTGAGGAGTACATGACCTGAG 2897  
QY 3458 CCAGTGTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3517  
Db 2898 CTCTCTACCTGCGATGATCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2957



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QY 3518 CTTCTTCTGACCCCTGGAGCCGGCATCTTGTATGTCCTGGCCGTATGACGGT 3577
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2958 GCTTCCTCTCTCCCTTTGGGGCCGCTTCTGTATCTCAGACGTTCTGGCCCTGCTGGC 3017
QY 3578 CGAGCTGTCGGCAGATGGCCCTCATPGGAATCAAGACATGCGCGTCCCTGGTCAT 3637
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3018 CCAGATCTTTGGGGCCCATGACTCTGCTGGCATCAAACTCTCGGCGCATTCGGGAGTCAT 3077
QY 3638 CCGTATGCTTCTGTTGGCATAGAGTGAATTCACCGCTTCAAGTTCGTTGGCTTCTT 3697
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3078 ACTCATCTTCAGCGCTGGGCGCATGATGCTGTGCTCATATGCTGATATCACTGGGCTTCAT 3137
QY 3698 GAGGGCCATGGGCGACAAAGACCCGAGGCTGTGCTTGGCCCTGGAGCACATGTTTGCACC 3757
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3138 GACATCTCGTTGGTGAACGACGACGCGCGCTCCAGCTGAGCATAGATGTCCCTGGAGACC 3197
QY 3758 CGTCTGATGATGGCGCCGCTGCTCAGTCTGGAGTGTGATGTCGCGCGGATCTGATTT 3817
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3198 ACTGTCTCAGCGCATGCTGACCTCCGGAGTGGCCGTGTTCAATGCTTCACGTCGCCCTT 3257
QY 3818 CGACTTCATTTGTAGATTTCTTCTTGTGCTGTGGCGATCTCACCATCTCGGCGCTTCT 3877
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3258 TGAATTTGTATCCGGGCACTTCTGCTGCTTCTGCTGTGATGCTTATGGCTTGGCGCTG 3317
QY 3878 CAATGGCTGCTTCTGCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3937
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3318 CAACAGCTTTGTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3377
QY 3938 TCCAGCGCAACGGCTTGAACCGCTGCGCACACCCCTCCCTGAGCACCCGCCAGC 3992
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Db 3378 GCCCGCTGAGCATCCAGACCCCATATTCACGCCCTCTCCGCTGCGCGCTGCGAGC 3432

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RESULT 11  
US-08-460-900C-42

Sequence 42, Application US/08460900C  
Patent No. 6165747

# GENERAL INFORMATION:

APPLICANT: Ingham, Phillip W.  
APPLICANT: McMahon, Andrew P.  
APPLICANT: Tabin, Clifford J.  
APPLICANT: Bunciot, David A.  
APPLICANT: Marti-Gorostiza, Elisa  
TITLE OF INVENTION: Vertebrate Embryonic Pattern-Inducing  
TITLE OF INVENTION: Proteins and Uses Related Thereto  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,900C  
FILING DATE: 5-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/435,093  
FILING DATE: 4-MAY-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/356,060  
FILING DATE: 14-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/176,427  
FILING DATE: 30-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Vincent, Matthew P.

```

; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: HMV-006.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3900 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3897
; US-08-460-900C-42

Query Match 7.8%; Score 411.8; DB 3; Length 3900;
Best Local Similarity 48.9%; Pred. No. 2,7e-89;
Matches 1730; Conservative 0; Mismatches 1542; Indels 263; Gaps 13;

QY 537 CGGCCAGCTACTGCGAGCCCGCTTCTGCTGAGCAGATTTCCAAAGGGAAGCTACT 596
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 82 CGCACCAGCTGGGTGGAGCCGCCAAGTGGCGCTGATCAGATAGATAGAGGCAAGCGCGT 141
QY 597 GACCGAAGAGCGCACTGCTGGGTGAGAGGGAAGTTTCAGAGACTCTTATTAACCTGGT 656
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 GCGACCCGCGAGCGCATCTATCTGCGATCAGTATTCACAGTCCCACTCGAAGCCCTGGC 201
QY 657 TGTTCATTTCAAAAAAAGTCTGCGCAAGTCTTGTGTTGCGGCCCTCATATTTGGGGCC 716
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Db 202 AGCTCGTGCAGAAAGCAGCCGCGCAAGTGTGCTATGCTGCTATCTGCTGCTGCTGCTG 261
QY 717 TTCGGGTGGATTTAAAGCAGCAGAACTCGAGACCAAGCTGAGAGGCTGTGGTGA 776
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 262 TTTCTCGTGGCTTAAGAGCGCCCGAGATCCACTCCAGTCCAGCAGCTGTGGATCAG 321
QY 777 GTTGGAGGAGCAGTAACTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 836
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Db 322 GAGGGCGCGGCTGAGAGCGGAGTGGCTTACACACAGAGAGCATGGCGAGAGAG 381
QY 837 ATGTTTAATCTCACTCATGTATACAGACCCCTTAAGAGAGAGTGTATGTCTGACC 896
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Db 382 TCGGCCAGCAGTACAGTCTGCTATTCAGAGCAGCCAGACCGGAGCGCTGCTGCTCAT 441
QY 897 ACAGAGGCTCTTACACACCTGAGCTGGGCTGAGGCTGAGGCGCGCTGTGCTATGATAC 956
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Db 442 CCGAGGCGCTGCTGCGCCAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 501
QY 957 ATGTACACAGGAGTGAATTTGGAACATTTGTGTACAAATCAGGAGAGC--TTATC 1013
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Db 502 CTCTACAGACCGAGATGGGGGCTGCGCGACATGTGCAACATGCGGAGACGCGCTCTTC 561
QY 1014 ACAGAAAGCTTACATGATGATGATTAATAGAAATATCTTACCTGTTGATTAATTA 1073
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Db 562 GAGGCACTACTACATGAGAGATCTGCGCCACCTCATCTGCTGCTGATCATCAGC 621
QY 1074 CTTTGGAGCTGCTTGGGAAGGGGAGAAATATACATGCGGAGACATACCTCT-- 1129
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 622 CCGCTGAGCTTTCTGGAAGGGAAGCCAGCTGTGGGTGCGGAATCAGCGGCTGTATTA 681
QY 1130 -----AGTTAAACCTCTTTGGGTGAGCAAACTTGCACCTTTGGAATCTCGGAAG 1184
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 682 CCAGGCTCAACCAAGCACTCTGTGAGCAACACTGAAATCCCGCTCTGTATGAGTAT 741
QY 1185 TTAAG-----AAATTAATCAATCAAGTGAAGCTGAGGGAAGT 1226
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 742 ATGAAGCAGAAAGATCTCCAGGAAAGATCACTTCACTTGAAGACCTGAGAGAGTAC 801
QY 1227 CTGAATTAAGCTGAGTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1286
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 802 ATGAAGCGTGGCGGCTATTCGAGTGGCTACATGAGAGAAAGCCCTGCTGAACCATGTAAT 861

```



Db	2838	CTGGCCCACTATCCATCCGGGCAATCCCTTCATCTTCTGGAGACATGACATGACCCTGGC	2897
Qy	3458	CCACGTGCGTGCCTGTATTATCAGCGTGGGTGGCTGCACATTCCTCGTGGCGCTGT	3517
Db	2898	CTCCCTACGAGCCATGATCTCGCCCTGGCGGTACTGCGCGCCCTGGTGGTCTCCCT	2957
Qy	3518	CTTCCCTTGCAACCCCTGGACGGCCGGGATCATTTGTATGGTCTCTGGCGGTATGACGGT	3577
Db	2958	GCTCCGCTCTCCGTTTGGGGCCGCCCTTCTCGTAICTATCAGCGTTTGGCCTGGCTGGC	3017
Qy	3578	CGAGCTGTTGGCAGATGATGGGCTCATCGGATCAAGCTCAGTCCCGTGGCCGTGTCAT	3637
Db	3018	CCGATATCTTTGGGGCCCATACTGCTGGGCATCAAACTCTCGGGCAATTCGGGACATAT	3077
Qy	3638	CGTGAATCGCTTCTGTTGGGATATAGAGATGAGATGACGTTCAACCGTTACAGTTGGCTTCT	3697
Db	3078	ACTCATCTCAGCGTGGGATGATGCTGTGCTTCATATGTCTGTATACATGGGCTTCAT	3137
Qy	3698	GACGGGCATCGGAGACAAAGCCAGGGGCTGTGCTTGGCCCTGGAGACATATGTTGGACCC	3757
Db	3138	GACATTCGGTTGGGAACCGAGAGCGCGCGTCACGCTGAGCATGCAGATGTCCTCGGGACCC	3197
Qy	3758	CGTCTCGATGGCGCCCGTGTCCACTCTGCTGGGAGTGTGATGCTGGCGGGATCTGAGTT	3817
Db	3198	ACTGTGCCAGGGCATCTACCTCCGAGAGGGCGGTTTCATGCTTCCACATGCGCCCTT	3257
Qy	3818	CGACTTCATATTCAGGATATTTCTTCTGTGCTGGGAGATCCTACACATTCGCGGCTTCT	3877
Db	3258	TGAGTTTGTGATCCGGCACTTGTGCTGGCTTGTGTGCTGTGTATATGCTTGGCGGCTTG	3317
Qy	3878	CATGGGCTGTGTTTGTCTTCCGTGCTTGTGTCTTCTTTGGACCATATCTGAGGTGTC	3937
Db	3318	CACACAGCCTTTGTGTGTCTCCCATCTTACGTAGACATGATGGGACCGGAGCGGAGCTGTG	3377
Qy	3938	TCCAGCGAAGGGCTTGAACCGCTGGCCACACCCCTCCCTGAGACCAACCCCGAC	3992
Db	3378	GCTCGCTGGACATCCAGACCGATATACAGGCCCTTCTCGGCTCGCTCGTGGAC	3432

RESULT 12  
US-08-540-406-5  
Sequence 5, Application US/08540406  
Patent No. 5837338  
GENERAL INFORMATION:  
APPLICANT: SCOTT, MATTHEW P  
APPLICANT: GOODRICH, LISA V  
APPLICANT: JOHNSON, RONALD L  
TITLE OF INVENTION: Patched Genes and their use  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
STREET: Four Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: CA  
COUNTRY: US  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,406  
FILING DATE: 06-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20015  
REFERENCE/DOCKET NUMBER: a60190-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-781-1989  
TELEFAX: 415-398-3249

```

: INFORMATION FOR SEQ ID NO: 5:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 4434 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:
:   MOLECULE TYPE: CDNA
:
: US-08-540-406-5

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Query Match	7.7%;	Score 405;	DB 2;	Length 4434;
Best Local Similarity	48.8%;	Pred. No. 1.2e-87;		
Matches 1711; Conservative	0;	Mismatches 1550;	Indels 246;	Gaps 13;

QY	537	CGGGCCAGCTACTGCGACCCCGGCTTCGCTCGTGGAGACGATTTCCAGAGGGGAAAGCTACT	596
Db	283	CGCACCACTGGGGTGGAGCGCCCAAGTGGCGCTGATCAGATTAAAGGCAAAAGCCGCT	342
QY	557	GGCCGGAAAGCCCACTGTGGCTGAGAGCGAAGTTTCAGAGACTCTTATTTAACTGGGT	656
Db	343	GGCACCCCGACGGCGATCTATTCGCATCGATATTCGATGCCACCTCCGAACCCCTGGGC	402
QY	657	TGTTTCATTTCAAAAAAGCGCGCAAGTTTCTGATGGGCGCCGTCATATTTGGGGCC	716
Db	403	AGCTCCGTCGCAAAAGACGCGGGCAAGGTCTATTTCGTGGCTATCTGGTGTAGACACC	462
QY	717	TTCCGGGGTGGATTAAAAAGCAGGAACCTCGAGACCAACCTGAGAGACTGTGGGTGAA	776
Db	463	TTCTCGTCGCGCTGGAAGACCGCCAGATCCACTCCAGAGGTGGACCAAGCTGTGATCCAG	522
QY	777	GTTGGAGGACGAGTAGTGTGATTAATTAATTATCTGCCAGAAATTGGAAAGAGCT	836
Db	523	GAGGGCGGGCGCTGGAGGCGAACTGGCCCTACACAGAAAGAGATCGCGAGAGACGAG	582
QY	837	ATGTTTAATCCCAACTCATGTATACAGACCCCTTAAGAAAGAGTGTATATGTCTCGAC	896
Db	583	TGCGGCACGCAATCAGTGTCTCATTCAGACGACCCAGACCCGGAAGCTCTCCGTCTGCAT	642
QY	897	ACAGAGCGCTCTTACACACCTTGAGACTGGCACTCCAGGCCGAGCCGTCGCATGTATAC	956
Db	643	CGGCGGGCGCTCTTCCCACTCGGAGGCTCTGGTCAAGGCCACCGCGCTCAAGGTGCAC	702
QY	957	ATGTCAACACGAGCAGGGAATTTGGAACTTTGTGTTACAAATTCAGAGAGAC---TATTC	1013
Db	703	CTCTACGACACCGAATGGGGGGCTCGCGCAATGTGTGCAACATGCCGACACGCGCTCTCTTC	762
QY	1014	ACAGAAACAGGTGTACATGTGATCAGATTAATAGAAATATCTTACCTGTTTGATTATTACA	1073
Db	763	GAGGCACTCTACTACATCAGAGAGATCTCGCGCACTCATTTCCGTCTCGATCATCAGC	822
QY	1074	CGTTTGGACTGCTTCTTGGGAAGGGCGGAATTACAGTCTTGGGACAGCATACCTCTCT	1129
Db	823	CGCGTGGACGTGTTTCTGGGAGGGAAGCCAGCTTTGGGTCCGGATACAGGGGTGTTATA	882
QY	1130	-----AGGTAACTCTCTTTGGGGTGGACAAACTTGGACCTTTTGAATTCCTGGAAAG	1184
Db	883	CCAGGCTCTCAACCAACGACTCTCTGTGAGCACCCTGTAATCCCGCTTGTGATCAGATAT	942
QY	1185	TTAA-----AGAAATTAACATATCACTGACAGCTGGAGGAATG	1228
Db	943	ATGAACCAAAAAGTGTCCGAGAAAAAGATCAGCTTGACTTCGAGACCCTGGACAGATAC	1002
QY	1227	CTGAATTAAGGCTGAGGTTGCTCATGTTTACATGAGACCGCCCTTCCTCAATTCGGCCGAT	1286
Db	1003	ATGAAGCGTGGCGCATTTGGCACTGGCTCATGTGAGAGAGCCCTTCGTAACCCCACTGAAT	1062
QY	1287	CCAGACTCGCCCGCCACACAGCCCCCAACAAAATTAACCAAAACCTCTTGTATATGCGCTT	1346
Db	1063	CCCAATTCCCGGACACGCGCACGGAACAAAGAACAGCACCCAGCGCGCGATGTGGAGCC	1122
QY	1347	GTTTGAATGCTGATGTCATGCGTTTATCCAGAACTATATGCACACTGGCAGAGAGAGTGG	1406
Db	1123	ATCCGTCGCGGAGGCTGCTACGGTTTATGGCGCCAGACACTGTGACGCGGAGAGACTGG	1182



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Db 3148 CTCGTGATCTCAGCGCTCTGCGCTCTGCGCCAGATCTTTGGGCCAATGACTCTGCTG 3207
QY 3606 GGAATCAAGCTCAGTCCGTGCGCCGTGATCTGATGCTTCTGTGGCATAGAGATG 3665
Db 3208 GGCATCAACACTCTGGCCATTTCCGCGAGTCATCTCTCAAGCGTGGCATGATGCTG 3267
QY 3666 GAGTTACACCGTTACGCTGCTTTGGCCCTTTGACGCGCATGCGGACAGAACGCCAGG 3725
Db 3268 TGCTTCATATGCTGATATCACTGGGCTTCATGACATTCGTTGCAACCGACGACGCCG 3327
QY 3726 GCTGCTGCTGCGCCGTGACACATGTTTGCACCCGCTCTGATGAGCGCCGCTGCTCACTG 3785
Db 3328 GTCCAGCTGACGATGACATGATGCTCTGGAGCCATTTGTCACGCAATGCTGACCTCGGA 3387
QY 3786 CTGGAGATGCTGATGCTGCGGATGATGATGCTGATGCTGATGCTGATGCTGCTGCTG 3845
Db 3388 GTGCGCGGTTCACTGCTCTCCACGTCGCGCTTTGAGTTTGTATCCGACACTTCTGCTG 3447
QY 3846 GTGCTGGGATCTTACCATCTGCGGCTTCTCAATGCGCTGTTTGGCTTCCGCTGCTT 3905
Db 3448 CTCTGCTGGGCTTCTTATGCTGCTGCGCTCTGCAACAGCTTTGTTGTTCCCATCTA 3507
QY 3906 TTGCTTCTTTGACACATATCTGAGGTGCTGCTGACGCAACGCGTGTGAACCGCTGCGC 3965
Db 3508 CTGAGCATGCTGGGACCGGAGCGGAGCTGCTGCGCTGAGACATCCAGACCGCATATCTC 3567
QY 3966 ACACCTTCCTGAGCCACCCCGCAGC 3992
Db 3568 ACGCCCTCTCGCTGCGCTGCGCAGC 3594

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## RESULT 13

US-08-656-055-5

Sequence 5, Application US/08656055

Patent No. 6027882

GENERAL INFORMATION:

APPLICANT: SCOTT, MATHEW P

APPLICANT: GOODRICH, LISA V

APPLICANT: JOHNSON, RONALD L

TITLE OF INVENTION: Patched Genes and their use

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Flehr, Hohbach, Test, Albritton &amp; Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/656, 055

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/540,406

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: a60190-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 4434 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear  
MOLECULE TYPE: cDNA  
US-08-656-055-5

Query Match 7.7%; Score 405; DB 3; Length 4434;  
Best Local Similarity 48.8%; Pred. No. 1.2e-87;

Matches 1711; Conservative 0; Mismatches 1550; Indels 246; Gaps 13;

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QY 537 CGGCCAGCTACTGCGACCGCGCTTCGCTGAGACGATTTCCAGAGGAGGCTACT 596
Db 283 CGCACACAGCTGGGTGAGCGCCCAAGTGGCGGTGATGATGATGATGATGATGATGATG 342
QY 597 GGGCGGAAAGCGCCAGTGTGCTGAGACGAACTTTCAGAACTCTTAATTAACCTGGT 656
Db 343 GGCAGCGGACAGGCGATCTATCTGATGATGATGATGATGATGATGATGATGATGATGAT 402
QY 657 TGTTCATTTCAAAAAAATCTGCGCAAGTCTTGGTGGGGCGCTTCATATTTGGGCGC 716
Db 403 AGCTCCGTGCAAAAGACAGCGCGGCAAGTCTATTCGTGCTATCTGCTGAGACAC 462
QY 717 TTGCGGTTGGGATTTAAAGACGCAACCTGAGACCAACGTTGAGAGACTGTGGTGAA 776
Db 463 TTCTGCGTGGCGTGAAGAGCGCCAGATCCACATCCAAAGTGTGACACAGCTGTGATCAG 522
QY 777 GTTGAAGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
Db 523 GAGGGGCGCGGCTGAGGCGGAACTGCGCTTACACACAGAAAGATGCGGAGAGACGAG 582
QY 837 ATGTTTAATCTCACTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 896
Db 583 TCGGCCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 642
QY 897 ACAGAGCGCTCTTACACACCTGAGACTGCGACCTCCAGCGCAGCGCTGCTCATGATAC 956
Db 643 CCGAGGCGGCTGCTTGGCCACCTGAGAGTCTGCTGCAAGGCGCGGCTGCAAGGTGAC 702
QY 957 ATGTACACAGGAGGAGTGAATTTGAACATTTGTTGTTGAACAATAGAGAGAGC---TTATC 1013
Db 703 CTCTACGACACCGAATGAGGGGCTGCGGACATGTCGCAACATGCCGAGACGCGCTTCC 762
QY 1014 ACAGAAACAGGTTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1073
Db 763 GAGGGCATCTACTACATGAGAGATCTGCGCACCTCATCTGCTGCTGATCATCAG 822
QY 1074 CCTTGGAGCTGCTTGGGAGGAGGGAATTTACAGTCTGGAGACGATACCTCT--- 1129
Db 823 CCGCTGAGCTGTTTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 882
QY 1130 -----AGTTAAACCTCTTGGCGGTGACAACTTGACCTTTGGAATTCCTGGAAGAG 1184
Db 883 CCAGGCTCAACCAACGACCTCTGTGAGCACCTGATCCCGCTGTGATGACATAT 942
QY 1185 TTTAA-----AGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1226
Db 943 ATGAACAAAGATGTCGAGAGAAAGATCACTGATGATGATGATGATGATGATGATGATGAT 1002
QY 1227 CTGAATTAAGCTGAGGTTGGTATGTTATGATGACGCGCCGCTGCTGATGAGGCGGAT 1286
Db 1003 ATGAAGCGTGGCGGCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1062
QY 1287 CCAGACTGCGCGCCAGACGCGCCCAACAAATTAACCAAACTTGTATGAGGCTT 1346
Db 1063 CCAATTTGCCGAGACGCGCACCGAACAAGACACCGAGCGCGGATGAGGAGGAGGAGGAGGAG 1122
QY 1347 GTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1406
Db 1123 ATCTGTCCGAGGAGGCTGCTACGCTTATGCGCGGAACACATGATGATGATGATGATGATGAT 1182
QY 1407 ATTGTGGTGGACAGATCAAGACAGCACTGGAATTAATCTGATGAGCGCCATGCGCTGACG 1466
Db 1183 ATTGTGGCGGAGCGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1242

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Qy	1467	ACATATGTCAGATTATATAGCTCCCAAGCAAAATGTAAGAGCACTTCAAGGGGATACAGGTAT	1526
Db	1243	TTCGGTGGGACACTATATGACCGAGAAAGAAATGTACAGCACTGGCAGGACAATACAAAG	1302
Qy	1537	GTCCTACACATCAACCTGGAACAGGAGCAAAAGCGGAGCCATCTGGAGGCTTGGCAGAG	1586
Db	1303	GTGGCAACATCTTGGATGGAACGAGGAGAAAGGACGGAGGATTTTGAACCTCTGGAGGCG	1362
Qy	1587	ACATATGTGGAGGTGGTTTCATAGAGTGTGCGACAGA-----CTCCACTCA	1634
Db	1363	AACCTTTTGGCGGAGAGCTGGAAACAGCTACGATTAACATTCGAGAAATTTGCCACAACCTAC	1422
Qy	1635	AAGGTGCTTTCCTTACACCCACAGACCCCTGGACAGCAATCTGAAATCTCTCTGACGTC	1694
Db	1423	GATATCTACGTGTTCAGCTCCGGCTGCACCTGGATGACATCTCGGCCAAAGTTCTCCATCCG	1482
Qy	1695	AGTGTATCCGCGTGGCCAGCGGCTACTTACTATGCTCGGCTATGCTCTGTCTAACCAATG	1754
Db	1483	AACGGCTTGTCCATATGTCACTGGCGCGTGGCCGTCACCGTTTGTATCCCTTTTGACAGCTC	1542
Qy	1755	CTGGCGT---GGGACGTGGTCAAAAGTCCCAAGGGTGGCGGCTGGCTGGCCGTCGTCG	1811
Db	1543	CTCCGCTGGAGGAGACCCGCTCCGTGGCCAGAGCAGTGTGGGCTGGCCCGGATTTCTGCTC	1602
Qy	1812	GTGTGCACTGTCAGTGGCTCAGAGACTGGGCGCTGTGCTCATTTGATGGAATTTCCCTTTAC	1871
Db	1603	ATGTGCTTCAGTACCGCCCGCGGATTTGGATTTGTCAAGCCCTCGTCGATACGTTTTCAT	1662
Qy	1872	GCTGCACACATCAGGTTTTTCCATTTTCGCTCTTGTTGGTGGTGGTGGATGATGTTTTT	1931
Db	1663	GGCGTGACCGT-----GCTATGGGGAGAGCAATGGCGGGAGCACAGCAAGCTG	1713
Qy	1932	CTTCTGGCCACCGCTTTCAGATCAACAGCAAGATAAAAGATTCCTTTTGAAGCAAG	1991
Db	1714	ATTCTCAAGAACGCCAGACACCCAGTGTTCCTTTTGGCCCTTGGTCTGGGCGCTC---	1770
Qy	1992	ACGGGGAGTGCCTGAAAGGACAGAGACCAAGCTGGCCCTCACTGCATACAGCAATGTC	2051
Db	1771	-----GATCACTACTTTCATATAGTGGAGCCAGGATCTCTGTTCAGTGGCTCAGACCGCA	1824
Qy	2052	ACAGCCTTCTTCATGGCCGCGGTAAATCCAAATTCGCGCTTGGGGCGGTCTCCCTCAG	2111
Db	1825	GGAATCTTCTTTCGGGCGGCTTATTTCCGTTGCCGCTTTGAAGATTTCTGCTGCAG	1884
Qy	2112	GCAGCGTACTAGTGTGTTTCAATTTTGGCATGTGTTCTGCTCATTTTTCCTGCAATTCCTC	2171
Db	1885	GCTGCCATCTTAATGTGCTCCAAATTTTGGCAGCGGCTATTTGTTTTCGGCCATATAT	1944
Qy	2172	AGCATGATTTAATATGACGCGAGGACAGAGATGATATTTTCTCTGTATTACAGC	2231
Qy	2232	CCCTGCGTGCAGAGAGTGAATTCAGGTTTGAACCTTAGGCTTACACCCGACACACAGCAAT	2291
Db	2002	CCGGTGTGAAGAAACAGCCGAAAGGTGGACACTCCGCTGTGCGCTGAACAAACAAAC	2061
Qy	2292	ACCGGCTACAGCCCCCACCACCCCTTACAGAGCCAGCTTTGGCCATGAAACGACATTT	2351
Db	2062	GGGCGGGGGGCCCGGCACTCCGAAGAGCTGCACACACA-----	2098
Qy	2352	ACCATGCAGTCCACTGTCCAGCTCCGACGAGAGTACAGACCCCAACAGCAGTGTACTAC	2411
Db	2099	-----	2098
Qy	2412	ACCACCGCTAGCGCGGCTCCGAGATCTCTGTGACGCCGTCACCGTGGACACAGGACAC	2471
Db	2099	-----ACAGGGTGGCGCTGCCGCC	2118
Qy	2472	CTCAGCTGCCAGAGCCAGAGAGCAGCAAGTCCCAAGAGGAACCTGCTCTCCAGTTTCTC	2531
Db	2119	CAGAAATCTCTGCTGTGAAGACAGAGGCGAGACATTCCTGTGGAGACAGTCACTGACGTGGCGTC	2178
Qy	2532	GACTCAGGCTCCAGCTCTGAGCCCCCTGTACGAAGTGGACATCTCATCTTTTGTCT	2591

[illegible]



Db 3208 GGCATCAACTCTGGCCATTCCGGCATCATCTCAGCGTGGGCATGATGCTG 3267  
 QY 3666 GAGTTCACCGTTACAGTCTTGGCTTTGACGGCCATCGCGCAAGAAGCCGAG 3725  
 Db 3368 TGCTTCATATGCTGATATCACTGGGCTTCAGATCCGTTGGCAACGACGCGCG 3327  
 QY 3726 GCTGTGCTGGCCCTGAGACACATGTTTGACCCGTCCTGGATGGCGCGTGTCCACTG 3785  
 Db 3328 GTCCAGCTGACCAATGATGCTCCGAGACCACTTGTCCAGCATGCTGACCTCGGA 3387  
 QY 3786 CTGGAGTGTGATGCTGGGAGATCTGATGCTGATGCTGATGCTGATGCTGCT 3845  
 Db 3388 GTGGCCGCTGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGCTG 3447  
 QY 3846 GTGCTGCGATCTGACCATCTCGGCTTCTCAATGGGCTGTTGCTGCTGCTGCT 3905  
 Db 3448 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3507  
 QY 3906 TTGCTTCTTGGACCATATCGAGGTGCTGACCAAGGCTTGACCGCTGCTGCT 3965  
 Db 3508 CTGAGCATGCTGAGCGAGCGAGCGAGCTGCTGCTGCTGAGCATCAGACCGCATATCC 3567  
 QY 3966 ACACTCTCCCTGAGCCACCCCGAGC 3992  
 Db 3568 ACGCCCTCTCCGCTGCGCGCTGCGAGC 3594

## RESULT 14

PCT-US95-13233-5  
 Sequence 5, Application PC/TUS9513233  
 GENERAL INFORMATION:  
 APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY  
 TITLE OF INVENTION: Patched Genes and their Use  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehm, Hobbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: US  
 ZIP: 94111  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13233  
 FILING DATE: 06-OCT-1990  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Berttram I  
 REGISTRATION NUMBER: 20015  
 REFERENCE/DOCKET NUMBER: a60190-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-781-1989  
 TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4434 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdna  
 PCT-US95-13233-5

Query Match Best Local Similarity 7.7%; Score 405; DB 4; Length 4434;

Matches 1711; Conservative 0; Mismatches 1550; Indels 246; Gaps 13;

OY 537 CGGCCAGCTCTGCGAGCGCGCTTGGCTCGAGGAGATTTCCAAAGGGAGGCTACT 596  
 || ||||| ||||| | || || ||||| ||||| || ||

Db 283 CGCACAGCTGGTGAGCGCCCAAGTGGCTCGATCAGATAGATAGAGGCAAGCGCGT 342  
 QY 597 GCGCGAAGAGCCGACCTGCTGAGAGGCAAGTTCAGAGACTCTTAACTATGAGT 656  
 Db 343 GCGAGCGGACAGGCGATCTATCTCGATCAGATATTCAGTCCACCTCGAAACCTTCGCG 402  
 QY 657 TGTTCATTCAAAAAAATCGCGCAAGTCTTGGTGTGGGCTCTCTATATTTGGGCG 716  
 Db 403 AGCTCCGCTGAAGAACAGCGGCGCAAGTGTCTATTCGCTATCTGCTGTGAGCAC 462  
 QY 717 TTGCGGTGGGATTAAGAACAGCACTCGACCTCGAGCCAGCTGAGAGCTGTGGTGA 776  
 Db 463 TTCTGCTGCGCTGGAAGAGCGCCAGATCCATCCAAAGTGACACACCTGTGATCCAG 522  
 QY 777 GTTGAAGAGCAGTAAGTCTGTAATTAATTAATCTGCGCCGAAGATTTGGAAGAGCT 836  
 Db 523 GAGGCGGCGCGCTGAGGCGAAGTGGCTACACAGAGAGATGCGGAGAGCAG 582  
 QY 837 ATGTTTAATCTCAACATGATACAGACCCCTTAAGAAAGAGTCTAATGTCTGAC 896  
 Db 583 TCGGCCACGATACGCTGCTATTCAGAGACCCAGACCCGAGACCGCTCGCTGAT 642  
 QY 897 ACAGAGCGCTCTTACAAACACCTGAGCTCGACCTCGAGGCGAGCGTCTCATGTATAC 956  
 Db 643 CCGCAGCGCTGCTTGGCCACCTGAGAGTCTGCTCAAGCCACCGCGTCAAGGTGAC 702  
 QY 957 ATGTACAAAGCAGTGGAAATTTGAACATTTGTTCACAAATCAGAGAGC---TTATC 1013  
 Db 703 CTCTACGACACCAATGCGGGGCTGCGCGACATGTGCAACATGCGGACAGCGCTCTTC 762  
 QY 1014 ACAGAAACAGGTACATGATGATATATGATATATCTTACCTTTGATATTTACA 1073  
 Db 763 GAGGCGATCTACATCTGACAGATCTGCGCACCTCTATCTGCTGATATACG 822  
 QY 1074 CCTTTGACTGCTCTGGAAGGCGCAATTAATGATGAGAGCAGATACCTCT--- 1129  
 Db 823 CCGCTGACTGTTTGGAGAGGAGCCAGCTGTTGGTCCGGAATCAGCGGCTGTTATA 882  
 QY 1130 -----AGTAAACCTCCTTTGGCGGTGACAACTTGCACCTTTGGAATTCGTAAGAG 1184  
 Db 883 CCAGGCTTCACCAACAGACTCTGAGACCCCTTAATCCCGCTCTGTGATGACTAT 942  
 QY 1185 TTAA-----AGAAATTAATCAAGTGAAGCAGCTGGAGAAATG 1226  
 Db 943 ATGAACAAGATGTCGAGAGAAAGATCAGCTTGAAGACCGTGAGAGCTAC 1002  
 QY 1227 CTGAATTAAGGCTGAGGTTGGTCAATGATGAGACCCCTGCTCAATCCGCGCAT 1286  
 Db 1003 ATGAAGCTGTGGGCTATGGGCTGATGAGAAAGCCCTGTGAACCCACTGAAT 1062  
 QY 1287 CCAGACTGCGCGCCACAGCGCCCAAGAAATTAACCAACCTCTTGAATGCGCTT 1346  
 Db 1063 CCCAATTCGCGGACAGCGACCGACCAAGAACAGACCCACCGCGGATGTGGAGCC 1122  
 QY 1347 GTTTGAATGTGATGCTTATTCAGAAATATATGATGAGAGGAGGAGT 1406  
 Db 1123 ATCTGTCCGAGGCTGTAGGTTATGCGGAGAACATCATCTGCGCGAGAGCTG 1182  
 QY 1407 ATGTGGGTGACAGTAAAGACAGCACTGGAATATCTGAGGCGCCATCCCTGAC 1466  
 Db 1183 ATTTGGCGGAGAGAGAGACCGAGCGACCTTGAAGAAAGCCAGCCCTGTGAG 1242  
 QY 1467 ACCATGTTCCAGTTAATGACTCCCAAGCAATGTGCGAGCACTTCAAGGGGTACAGAT 1526  
 Db 1243 TCGGTGTGAGCTGATGATGAGAGAGAAATGTACGACCACTGCGAGACAACTAAG 1302  
 QY 1527 GTTCACACATCAACTGAGAGAGACAAAGCGGACCATCTGAGAGCTTGGAGAG 1586  
 Db 1303 GTGCACCATCTTGGATGAGAGAGAGAGAGAGGAGGAGGTTTGAAGCGCTTGGAGCGC 1362  
 QY 1587 ACATATGTGAGAGGTCTTCAAGACAGTGTGCGACAGAA-----CTCCACTCA 1634  
 Db 1363 AACTTTTCGGGAGAGTGAACAGCTCTACGTAAACAGTTCAGAAATTCACCAACTAC 1422

QY 1635 AAGGTGCTTCTTCAACACACACACCCCTGGAGACATCTCGAATCTTCTGACATC 1694  
 Db 1423 GATATCTACGTGTTACAGCTGGCTGCGATGATGACATCTGGCCAAAGTCTCCATGCC 1482  
 QY 1695 AGTGTATCCGCGGTGGCCAGCGGCTACTATCTCATGCTGCTGCTGCTGCTGCTGCTG 1754  
 Db 1483 AGCGCTTGTTCATGTCATGTCGCGGTGGCGCTGACCGCTTTGTATGCTTTTGACGCTC 1542  
 QY 1755 CTGCGCT---GGACCTGCTCAAGTCCGAGGGTCCGTTGGGGGCTGGGCTGCTGCTG 1811  
 Db 1543 CTGCGCTGGAGAGACCCGCTGCTGCGCAGACAGTGTGGCGGCTGGCGGAGTCTGCTC 1602  
 QY 1812 GTTGCATGTCAGTGTGTCAGAGTGGGCTGTGCTCATGATGATGATGATGATGATGATG 1871  
 Db 1603 ATGTCGTTCACTACCGCGCGCGGATGGATGTCAGCGCTGCTGCTGCTGCTGCTGCTG 1662  
 QY 1872 GCTGCACACACTCAGGTTTCCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1931  
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# RESULT 15

US-08-540-406-7  
 : Sequence 7, Application US/08540406  
 : Patent No. 5837538

GENERAL INFORMATION:  
 : APPLICANT: SCOTT, MATHEW P  
 : APPLICANT: GOODRICH, LISA V  
 : APPLICANT: JOHNSON, RONALD L  
 : TITLE OF INVENTION: Patched Genes and their Use  
 : NUMBER OF SEQUENCES: 19  
 : CORRESPONDENCE ADDRESS:

ADDRESS: Flehr, Hohbach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: CA

COUNTRY: US  
 ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/540,406  
 FILING DATE: 06-OCT-1995  
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertiam I  
 REGISTRATION NUMBER: 20015  
 REFERENCE/DOCKET NUMBER: a60190-1  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989  
 TELEFAX: 415-398-3249  
 INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 345 base pairs  
 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-540-406-7

Query Match 1.5%; Score 77; DB 2; Length 345;  
 Best Local Similarity 51.2%; Pred. No. 1.9e-09;  
 Matches 176; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

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Search completed: January 13, 2001, 09:20:03  
 Job time: 11106 sec



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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

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1	5288	100.0	5288	13	US-08-954-655-18	Sequence 18, App
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3	5288	100.0	5288	13	US-08-954-701A-18	Sequence 18, App
4	4684.8	88.6	6568	12	US-08-954-636-11	Sequence 1, App
5	3801.2	71.9	5187	13	US-08-954-655-3	Sequence 3, App
6	3801.2	71.9	5187	13	US-08-954-665-9	Sequence 9, App
7	3801.2	71.9	5187	13	US-08-954-668-3	Sequence 3, App
8	3801.2	71.9	5187	13	US-08-954-701A-3	Sequence 9, App
9	3801.2	71.9	5187	13	US-08-954-701A-9	Sequence 9, App
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11	1176.4	22.2	4030	14	US-09-060-939A-1	Sequence 1, App
12	1176.4	22.2	4030	16	US-09-293-505-1	Sequence 1, App
13	1173.2	22.2	4391	16	US-09-207-857-1	Sequence 1, App
14	593.8	11.2	2082	14	US-09-060-939A-9	Sequence 1, App
15	593.8	11.2	2082	16	US-09-293-505-9	Sequence 9, App
16	472.2	8.9	1734	12	US-08-857-636-58	Sequence 58, App
17	450.2	8.5	3861	42	US-60-171-625-89	Sequence 89, App
18	450.2	8.5	3861	42	US-60-173-464-3397	Sequence 3397, App
19	450.2	8.5	3861	44	US-60-191-637-0882	Sequence 4082, App
20	450.2	8.5	3861	44	US-60-191-661-3260	Sequence 3260, App
21	450.2	8.5	3861	46	US-60-219-005-44	Sequence 44, App
22	449	8.5	485	16	US-09-235-076-21578	Sequence 21578, App
23	449	8.5	485	17	US-09-289-768-26469	Sequence 26469, App
24	449	8.5	485	17	US-09-332-782-21578	Sequence 21578, App
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26	433.8	8.2	2032	19	US-09-500-063-1	Sequence 1, App
27	427.2	8.1	445	14	US-09-036-521A-1124	Sequence 1124, App
28	420.2	7.9	3900	8	US-08-462-900A-42	Sequence 110, App
29	411.8	7.8	3900	10	US-08-674-509B-42	Sequence 42, App
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33	411.8	7.8	3900	13	US-08-954-771-42	Sequence 42, App
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44	390.4	7.4	482	16	US-09-287-618-5277	Sequence 5277, App
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QY	3061	GGGATTAAGCCCATGCGACATCACCGACAGTTTGACTTAAACAGCGTGGTGTGATGAGATGGCA	3120
Db	3061	GGGATTAAGCCCATGCGACATCACCGACAGTTTGACTTAAACAGCGTGGTGTGATGAGATGGCA	3120
QY	3121	TCATTTAATCCAGGCGCTTTTCTACATCTACTTACAGGCTTGGGTGACGAACGACCCGCTGC	3180
Db	3121	TCATTTAATCCAGGCGCTTTTCTACATCTACTTACAGGCTTGGGTGACGAACGACCCGCTGC	3180
QY	3181	CGTATGCTGCCCTCCAGGGCAACATTCGGGCAACCGACGACGAAATGAGGTGCACGCAAAAG	3240
Db	3181	CGTATGCTGCCCTCCAGGGCAACATTCGGGCAACCGACGACGAAATGAGGTGCACGCAAAAG	3240
QY	3241	CCGACTACATGCTTAAACCAAGGCTGAGAAATCCCGGACAGAACGCCCATCGAGTATGCC	3300
Db	3241	CCGACTACATGCTTAAACCAAGGCTGAGAAATCCCGGACAGAACGCCCATCGAGTATGCC	3300
QY	3301	AGTTCTCCTTTTACTCTCAACGGGTTGGGGACACTCAAGACTTTTGTGAGGCAATTGGAA	3360
Db	3301	AGTTCTCCTTTTACTCTCAACGGGTTGGGGACACTCAAGACTTTTGTGAGGCAATTGGAA	3360
QY	3361	AAGTAAGGACCATTCGACAGCAACTATACGAGCTTGGGCTGTGCAGTTAACCCAACGGCT	3420
Db	3361	AAGTAAGGACCATTCGACAGCAACTATACGAGCTTGGGCTGTGCAGTTAACCCAACGGCT	3420
QY	3421	ACCCCTTCCTTTCGAGAGAGTACATTCGGGCTCCGACATGCGTGCATGCTTCAATCA	3480
Db	3421	ACCCCTTCCTTTCGAGAGAGTACATTCGGGCTCCGACATGCGTGCATGCTTCAATCA	3480
QY	3481	GGGTGTGTGGCTGCACTTCTCTGTGTGCGCTTCTCTTCTGAAACCCCTTGAGCGG	3540
Db	3481	GGGTGTGTGGCTGCACTTCTCTGTGTGCGCTTCTCTTCTGAAACCCCTTGAGCGG	3540
QY	3541	CGGGATATATTGTATGTCTCTGGGCGTGAATGACGCTGTGTCGGCAATGATGGGCC	3600
Db	3541	CGGGATATATTGTATGTCTCTGGGCGTGAATGACGCTGTGTCGGCAATGATGGGCC	3600
QY	3601	TCATATCGAATCAAGCTACGTGCCGAGCCCGTGGTATCTCTATGCGCTTCTGTGGCATAG	3660
Db	3601	TCATATCGAATCAAGCTACGTGCCGAGCCCGTGGTATCTCTATGCGCTTCTGTGGCATAG	3660
QY	3661	GAGTGAAGTTCACCGTTCACGTGCTTGTGGCTTTCTGACGCGCAATCGGCAACAAGAACCC	3720

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|||||
Db 3661 GAGTGGAGTTACCGTTCACGTTGGCTTTGCGCTTCTGACGGCCATCGGCGAACAAGACC 3720
|||
Qy 3721 GCAGGGCTGTCTTCCCTTGAGACACATGTTTGCACCCGCTCTGATGGCCGCTGTCCA 3780
|||
Db 3721 GCAGGGCTGTCTTCCCTTGAGACACATGTTTGCACCCGCTCTGATGGCCGCTGTCCA 3780
|||
Qy 3781 CTCTGCTGGAGTGTCTGATGCTGGGGGATCTGATGCTGACTTTCATTTGACGATTTTCT 3840
|||
Db 3781 CTCTGCTGGAGTGTCTGATGCTGGGGGATCTGATGCTGACTTTCATTTGACGATTTTCT 3840
|||
Qy 3841 TTGCTGTGCTGGCATCTCTCAACCATCTCGGCGTTCTCAATGGGCTGTTTGTCTCCG 3900
|||
Db 3841 TTGCTGTGCTGGCATCTCTCAACCATCTCGGCGTTCTCAATGGGCTGTTTGTCTCCG 3900
|||
Qy 3901 TGCTTTTGTCTTTCTTTGGACCATATCTGAGTGTCTCCACCAACGGCTTGAAACCGCC 3960
|||
Db 3901 TGCTTTTGTCTTTCTTTGGACCATATCTGAGTGTCTCCACCAACGGCTTGAAACCGCC 3960
|||
Qy 3961 TGCCACACCCCTCCCTGAGCCACCCCGAGGCTGGTCCGCTTGCCATGCGCCGCGCC 4020
|||
Db 3961 TGCCACACCCCTCCCTGAGCCACCCCGAGGCTGGTCCGCTTGCCATGCGCCGCGCC 4020
|||
Qy 4021 ACACGACAGGGGCTGTATTCCTCCGACTCGGAGTATAGTTCCAGACAGACGTCTAG 4080
|||
Db 4021 ACACGACAGGGGCTGTATTCCTCCGACTCGGAGTATAGTTCCAGACAGACGTCTAG 4080
|||
Qy 4081 GCCCTACGAGGAGTGTGGGCACTACGAGGCCAGAGGGCCGGGAGGCGCCGCCACC 4140
|||
Db 4081 GCCCTACGAGGAGTGTGGGCACTACGAGGCCAGAGGGCCGGGAGGCGCCGCCACC 4140
|||
Qy 4141 AAGTATGTGTGAAGACACAGAAACCCGCTTGCCGCACTGCTGATGTGTCATCCG 4200
|||
Db 4141 AAGTATGTGTGAAGACACAGAAACCCGCTTGCCGCACTGCTGATGTGTCATCCG 4200
|||
Qy 4201 AATCCAGGATCACCACCTCTGAAACCCGAGACAGACCCCACTGAGTCAAGGCTCC 4260
|||
Db 4201 AATCCAGGATCACCACCTCTGAAACCCGAGACAGACCCCACTGAGTCAAGGCTCC 4260
|||
Qy 4261 TGCCCTCCGGAGGGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 4320
|||
Db 4261 TGCCCTCCGGAGGGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 4320
|||
Qy 4321 CACCCCTCTACAGACCGGCGGAGAGCGCTTTTGAATTTCTACTGAAGGCACTTCTGCC 4380
|||
Db 4321 CACCCCTCTACAGACCGGCGGAGAGCGCTTTTGAATTTCTACTGAAGGCACTTCTGCC 4380
|||
Qy 4381 CTAGCAATAGGGCCGCTGGGGCCCTCGGCGGGCCGCTTCTCAACCCCTCGGAACCCAG 4440
|||
Db 4381 CTAGCAATAGGGCCGCTGGGGCCCTCGGCGGGCCGCTTCTCAACCCCTCGGAACCCAG 4440
|||
Qy 4441 CTTCCACTGCGCATGGGAGGCTCGGCGGGGCTGAGTGGCCAGCCATCAGACGTGACG 4500
|||
Db 4441 CTTCCACTGCGCATGGGAGGCTCGGCGGGGCTGAGTGGCCAGCCATCAGACGTGACG 4500
|||
Qy 4501 CTTTGCCTCCGTTGATGTGCGCTGACCCGCGCTGTCTGAGGCGCTGGGCGGAGACC 4560
|||
Db 4501 CTTTGCCTCCGTTGATGTGCGCTGACCCGCGCTGTCTGAGGCGCTGGGCGGAGACC 4560
|||
Qy 4561 CCGGAGGGGAGCTGTGCCAGGCTACCCCTGAGACTGACACGCGCTGTTTGAAGACCCCC 4620
|||
Db 4561 CCGGAGGGGAGCTGTGCCAGGCTACCCCTGAGACTGACACGCGCTGTTTGAAGACCCCC 4620
|||
Qy 4621 ACGTCCCTTTCCAGTCCGCTGTGAGAGGAGGATTCGAAGGAGGAGTTCATTTGACCTGC 4680
|||
Db 4621 ACGTCCCTTTCCAGTCCGCTGTGAGAGGAGGATTCGAAGGAGGAGTTCATTTGACCTGC 4680
|||
Qy 4681 AGGAGCTGGAATCGAGAGAGGCGCGGAGAGCACTCAACTAGAGGTGATTAAT 4740
|||
Db 4681 AGGAGCTGGAATCGAGAGAGGCGCGGAGAGCACTCAACTAGAGGTGATTAAT 4740
|||
Qy 4741 CTGAAGCAAGAGGCGCAAGATTTGAACCCCGCACCCCTCTTTCCAGAACTGCTT 4800
|||

```

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Db 4741 CTGAAGCAAGAGGCGCAAGATTTGAACCCCGCACCCCTCTTTCCAGAACTGCTT 4800
|||
Qy 4801 GAAGAGAACTGTGGAGTTATGAGAAAGATGCCCTGAGGAGACAGACAGTTCATTTT 4860
|||
Db 4801 GAAGAGAACTGTGGAGTTATGAGAAAGATGCCCTGAGGAGACAGACAGTTCATTTT 4860
|||
Qy 4861 ACTGAACCGATTTGTTATTTTGTAAATTTCTATTAATTTTAAAGATGTACACA 4920
|||
Db 4861 ACTGAACCGATTTGTTATTTTGTAAATTTCTATTAATTTTAAAGATGTACACA 4920
|||
Qy 4921 TGTGTATATATAGAGAGAGATGTAAGTGTATGATCTGGGCTTCTCCACTCTGCC 4980
|||
Db 4921 TGTGTATATATAGAGAGAGATGTAAGTGTATGATCTGGGCTTCTCCACTCTGCC 4980
|||
Qy 4981 CCAAGAGTGTGAGGCGCACAGAGGGGCGCTCCGATTTTGTGATTTGGGCTCCGTCACA 5040
|||
Db 4981 CCAAGAGTGTGAGGCGCACAGAGGGGCGCTCCGATTTTGTGATTTGGGCTCCGTCACA 5040
|||
Qy 5041 ACCAAGCTTCAATAGTCTTAAATTTTCAACATATGCTGCTGCTTAAATATTTATAT 5100
|||
Db 5041 ACCAAGCTTCAATAGTCTTAAATTTTCAACATATGCTGCTGCTTAAATATTTATAT 5100
|||
Qy 5101 TTACTTGTATATATCTATGCAATATGCTTATGTAATAGATTTTGTGAAGGTTTC 5160
|||
Db 5101 TTACTTGTATATATCTATGCAAAATTTGCTTATGTAATAGATTTTGTGAAGGTTTC 5160
|||
Qy 5161 TGTTTAAATATTTTAAATTTTGCATATCCAAACCCCTGGTATGTAATGTAATGTTACTGTT 5220
|||
Db 5161 TGTTTAAATATTTTAAATTTTGCATATCCAAACCCCTGGTATGTAATGTAATGTTACTGTT 5220
|||
Qy 5221 AACTTTCAACACGCTATGCTGATTAATTTTGTAAATGAGCAGATATGAAAGAAC 5280
|||
Db 5221 AACTTTCAACACGCTATGCTGATTAATTTTGTAAATGAGCAGATATGAAAGAAC 5280
|||
Qy 5281 CCGGAATT 5288
|||
Db 5281 CCGGAATT 5288
|||

RESULT 2
US-08-954-668-18
? Sequence 18, Application US/08954668
? GENERAL INFORMATION:
? APPLICANT: SCOTT, MATHEW P
? APPLICANT: GOODRICH, LISA V
? APPLICANT: JOHNSON, RONALD L
? TITLE OF INVENTION: Patched Genes and their use
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Foley, Hoag & Eliot
? STREET: One Post Office Square
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: ASCII(text)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/954,668
? FILING DATE: 20-Oct-1997
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: Vincent, Matthew P.
? REGISTRATION NUMBER: 36709
? REFERENCE/DOCKET NUMBER: SUV-003,06
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-832-1000
? TELEFAX: 617-832-7000
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:

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LENGTH: 5288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
us-08-954-668-18

Query Match 100.0%; Score 5288; DB 13; Length 5288;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCGGGGGACCGCAAGAGTCCCGGGGAAGCCCGCAAGACAGCGTCCGCGCC 60  
DB 1 GAATTCGGGGGACCGCAAGAGTCCCGGGGAAGCCCGCAAGACAGCGTCCGCGCC 60  
QY 61 GCCGCGCTCTGCTCTTCCGCAACGTGATGCGGAGCGCGCGCCGACAGACCTTGCGGA 120  
DB 61 GCCGCGCTCTGCTCTTCCGCAACGTGATGCGGAGCGCGCGCCGACAGACCTTGCGGA 120  
QY 121 CCCCCCGCAATGTGCAAGTGAAGCGCCAGGGTCTGACTCCCGGACGCGCGCGCC 180  
DB 121 CCCCCCGCAATGTGCAAGTGAAGCGCCAGGGTCTGACTCCCGGACGCGCGCGCC 180  
QY 181 GCAGCGGACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
DB 181 GCAGCGGACAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
QY 241 CGAGCCCGACAGCGCTCGCGCCAGCGGTCTCTGCAAGCCGAGCGCCGAGCGCCAG 300  
DB 241 CGAGCCCGACAGCGCTCGCGCCAGCGGTCTCTGCAAGCCGAGCGCCGAGCGCCAG 300  
QY 301 GAGCCCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
DB 301 GAGCCCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360  
QY 361 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
DB 361 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
QY 421 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
DB 421 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
QY 481 GCAGACGAGCGGGGGGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
DB 481 GCAGACGAGCGGGGGGCGTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540  
QY 541 CCAGCTACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600  
DB 541 CCAGCTACTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600  
QY 601 GCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
DB 601 GCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660  
QY 661 ACATTTAAAAAACTGCGGCAAGTTCTTGTGTTGCGCTCTCAATTTTGGGGCGCTTGC 720  
DB 661 ACATTTAAAAAACTGCGGCAAGTTCTTGTGTTGCGCTCTCAATTTTGGGGCGCTTGC 720  
QY 721 CGGTGGGATTTAAAGCGCAACTCGAGACCAAGTGGAGAGTGTGGGGGAAATTGG 780  
DB 721 CGGTGGGATTTAAAGCGCAACTCGAGACCAAGTGGAGAGTGTGGGGGAAATTGG 780  
QY 781 GAGGACGAGTAAAGTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
DB 781 GAGGACGAGTAAAGTGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840  
QY 841 TTAATCTCAATCTATGATACAGACCCCTAAAGAAAGGTCATGTCCTGACACACAG 900  
DB 841 TTAATCTCAATCTATGATACAGACCCCTAAAGAAAGGTCATGTCCTGACACACAG 900  
QY 901 AAGCGCTCTACAAACCTGAGACTCGGACCTCCAGGCGCAGCGCTCATGTATACATGT 960

DB 901 AAGCGCTCTACAAACCTGAGACTCGGACCTCCAGGCGCAGCGCTCATGTATACATGT 960  
QY 961 ACAACAGGCGAGTGAATTTGGAACATTTGGTTTACAAATACAGGAGACTTATCCACAAA 1020  
DB 961 ACAACAGGCGAGTGAATTTGGAACATTTGGTTTACAAATACAGGAGACTTATCCACAAA 1020  
QY 1021 CAGGTTTACATGATCATATATATATATATATATATATATATATATATATATATATATAT 1080  
DB 1021 CAGGTTTACATGATCATATATATATATATATATATATATATATATATATATATATAT 1080  
QY 1081 ACTGCTTCTGGAAGGCGGCAATTTACAGTCTGGGACAGCATACCTCTAGTAAACCTC 1140  
DB 1081 ACTGCTTCTGGAAGGCGGCAATTTACAGTCTGGGACAGCATACCTCTAGTAAACCTC 1140  
QY 1141 CTTTGGGCGGCAAACTTCGACCCCTTGGAAATTTCTCGGAAGAGTTTAAAGAAATTAAC 1200  
DB 1141 CTTTGGGCGGCAAACTTCGACCCCTTGGAAATTTCTCGGAAGAGTTTAAAGAAATTAAC 1200  
QY 1201 ATCAAGTGGACAGTGGGAGAAATGCTGAATTAAGGCTGAGTGTGATGTATACATGG 1260  
DB 1201 ATCAAGTGGACAGTGGGAGAAATGCTGAATTAAGGCTGAGTGTGATGTATACATGG 1260  
QY 1261 ACCGCCCTGCTCAATCCGCGCGATCCAGACTGCCCGCCAGAGCCCGCAACAAAATT 1320  
DB 1261 ACCGCCCTGCTCAATCCGCGCGATCCAGACTGCCCGCCAGAGCCCGCAACAAAATT 1320  
QY 1321 CAACCAAACTTGTATATATATATATATATATATATATATATATATATATATATATAT 1380  
DB 1321 CAACCAAACTTGTATATATATATATATATATATATATATATATATATATATATATAT 1380  
QY 1381 AGTATATACATGAGAGAGAGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
DB 1381 AGTATATACATGAGAGAGAGTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440  
QY 1441 AACTGTGAGCGCCATGCGCTGACAGACATGTTCCAGTTAATGATCTCCCAAGCAATGT 1500  
DB 1441 AACTGTGAGCGCCATGCGCTGACAGACATGTTCCAGTTAATGATCTCCCAAGCAATGT 1500  
QY 1501 ACGAGCACTTCAAGGGGATGCGATATGCTCAACATCAACATCGAAGTGAAGAGAGAGAG 1560  
DB 1501 ACGAGCACTTCAAGGGGATGCGATATGCTCAACATCAACATCGAAGTGAAGAGAGAGAG 1560  
QY 1561 CAGCCATCTGGAGGCGCTGGGAGAGACATATGAGAGGTTGATCATCAGAGTGTGCAC 1620  
DB 1561 CAGCCATCTGGAGGCGCTGGGAGAGACATATGAGAGGTTGATCATCAGAGTGTGCAC 1620  
QY 1621 AGAATCTCAGTCAAAAAGGCTTTCTTCCACACACAGACCTGAGACATCTGAAAT 1680  
DB 1621 AGAATCTCAGTCAAAAAGGCTTTCTTCCACACACAGACCTGAGACATCTGAAAT 1680  
QY 1681 CTTTCTCTGAGCTGAGTGTGATGCGGCGGAGGCGGCACTTACATCATCTGCGCTATG 1740  
DB 1681 CTTTCTCTGAGCTGAGTGTGATGCGGCGGAGGCGGCACTTACATCATCTGCGCTATG 1740  
QY 1741 CCTGTCTAACCATGCTGGGCTGGGAGTGTCTCCAAAGTCCCAAGGTTGGCGTGGGCTG 1800  
DB 1741 CCTGTCTAACCATGCTGGGCTGGGAGTGTCTCCAAAGTCCCAAGGTTGGCGTGGGCTG 1800  
QY 1801 GCGTCTCTGCTGGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1860  
DB 1801 GCGTCTCTGCTGGTGTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1860  
QY 1861 TTTCTTCTTAAAGCTCAACCACTCAAGGTTTGGCAATTTCTGCGCTTGGTGTGGTGTG 1920  
DB 1861 TTTCTTCTTAAAGCTCAACCACTCAAGGTTTGGCAATTTCTGCGCTTGGTGTGGTGTG 1920  
QY 1921 ATGATGTTTCTTCTTCTGCGCCAGCGCTTCAAGTGAAGAGAGTGAAGTGAAGTGAAGT 1980  
DB 1921 ATGATGTTTCTTCTTCTGCGCCAGCGCTTCAAGTGAAGAGAGTGAAGTGAAGTGAAGT 1980  
QY 1981 TTGAGGACAGGACCGGGGAGTGTGAGAGCGCAGAGAGAGCGTGTGCGCTCAGTCA 2040

Db 1981 TTGAGCAGAGACCGGGGAGTGCCTGAAGCGCACAGAGCCAGCGTGCGCTCAGCTCCA 2040  
QY 2041 TCAGCATGTACAGCCTTCTTCATGCGCGGTTAATCCCAATTCGCCGTCTGCGGGCT 2100  
Db 2041 TCAGCAATGTACAGCCTTCTTCATGCGCGGTTAATCCCAATTCGCCGTCTGCGGGCT 2100  
QY 2101 TCTCCCTCCAGGAGCGGTACTAGGTGTCTCAATTTTGGCATTTGCTGCTCATTTTTC 2160  
Db 2101 TCTCCCTCCAGGAGCGGTACTAGGTGTCTCAATTTTGGCATTTGCTGCTCATTTTTC 2160  
QY 2161 CTGCAATTTCTCAGCATGGATTTATATGACGCGAGAGACGAGATGATTTTCTGCT 2220  
Db 2161 CTGCAATTTCTCAGCATGGATTTATATGACGCGAGAGACGAGATGATTTTCTGCT 2220  
QY 2221 GTTTTAAAGCCCTGGCTCAGAGAGTGAATTCAGTTGAACCTCAGGCTCAGCGACA 2280  
Db 2221 GTTTTAAAGCCCTGGCTCAGAGAGTGAATTCAGTTGAACCTCAGGCTCAGCGACA 2280  
QY 2281 CACAGCAATATACCGGCTACAGCCGCCACGCTCCCTACAGCAGCCAGCTTTGGCCATG 2340  
Db 2281 CACAGCAATATACCGGCTACAGCCGCCACGCTCCCTACAGCAGCCAGCTTTGGCCATG 2340  
QY 2341 AAACGCGAATTTACATGCACTGCTCAGCTGTCCAGCAGAGATACGACCCACACGC 2400  
Db 2341 AAACGCGAATTTACATGCACTGCTCAGCTGTCCAGCAGAGATACGACCCACACGC 2400  
QY 2401 ACGTGTACTACACACCGCTGAGCGGCTCCGAGATCCTGTGACGCGCTCAGCGTGA 2460  
Db 2401 ACGTGTACTACACACCGCTGAGCGGCTCCGAGATCCTGTGACGCGCTCAGCGTGA 2460  
QY 2461 CACAGCAACCCCTGACGTCCAGAGACCAGAGAGCAGCAGCTCCACAAAGGAGCCTGCTCT 2520  
Db 2461 CACAGCAACCCCTGACGTCCAGAGACCAGAGAGCAGCAGCTCCACAAAGGAGCCTGCTCT 2520  
QY 2521 CCCAGTCTCCGAGTCCAGGCTCCAGCTGCTGAGCAGCCGCCCTGTAGAGTGAAGTGA 2580  
Db 2521 CCCAGTCTCCGAGTCCAGGCTCCAGCTGCTGAGCAGCCGCCCTGTAGAGTGAAGTGA 2580  
QY 2581 CATCTTTTGTGAGAGACGACTATGCTCTTCTTGAACCAAAAGCAGAGTGTGTG 2640  
Db 2581 CATCTTTTGTGAGAGACGACTATGCTCTTCTTGAACCAAAAGCAGAGTGTGTG 2640  
QY 2641 TGATCTTCTTCTTCTGAGGCTGCTGAGGAGTCAAGCCTTTATGAGCACACCGCAGTGA 2700  
Db 2641 TGATCTTCTTCTTCTGAGGCTGCTGAGGAGTCAAGCCTTTATGAGCACACCGCAGTGA 2700  
QY 2701 ACGGAGCTGAGACCTTACGAGACATGTACTCGGGAACCAAGAAATATGATTTATGCTG 2760  
Db 2701 ACGGAGCTGAGACCTTACGAGACATGTACTCGGGAACCAAGAAATATGATTTATGCTG 2760  
QY 2761 CACAATTCAAATACCTTCTTCTTCAACATGTATATAGTACCCAGAAAGCAGACTACC 2820  
Db 2761 CACAATTCAAATACCTTCTTCTTCAACATGTATATAGTACCCAGAAAGCAGACTACC 2820  
QY 2821 CGAATATTCACACACTTACTTACGACTACACAGAGATTGAGTAACTGTAAGTATGTCA 2880  
Db 2821 CGAATATTCACACACTTACTTACGACTACACAGAGATTGAGTAACTGTAAGTATGTCA 2880  
QY 2881 TGTGGAAGAAACAAAGAGCTTCCCAAAATGTGCTGACATTCCTCAAGAGATGCTCTTC 2940  
Db 2881 TGTGGAAGAAACAAAGAGCTTCCCAAAATGTGCTGACATTCCTCAAGAGATGCTCTTC 2940  
QY 2941 AGGAGACTCAGAGATCATTTGACAGTGAAGTGAAGAAACCGGAAATCATGCGCAAAAT 3000  
Db 2941 AGGAGACTCAGAGATCATTTGACAGTGAAGTGAAGAAACCGGAAATCATGCGCAAAAT 3000  
QY 3001 ACAAGAAATGATCAGACGATGAGTCTGCTTACAAACTCCTGTGCAAAACCGGAGCC 3060  
Db 3001 ACAAGAAATGATCAGACGATGAGTCTGCTTACAAACTCCTGTGCAAAACCGGAGCC 3060  
QY 3061 GCGATTAAGCCCATGACATCAGCCAGTGTGACTTAACAGGCTGTGAGTGAAGTGA 3120  
Db 3061 GCGATTAAGCCCATGACATCAGCCAGTGTGACTTAACAGGCTGTGAGTGAAGTGA 3120

QY 3121 TCATTAATCCAGAGGCTTCTTACATTCACCTGACGAGGCTTGAGGCTCAGCAAGCCCGTGC 3180  
Db 3121 TCATTAATCCAGAGGCTTCTTACATTCACCTGACGAGGCTTGAGGCTCAGCAAGCCCGTGC 3180  
QY 3181 CGTATGCTGCTCCAGGAGCAACATCCGAGCAGACCCAGACGAAATGGGTCCAGCAAAAG 3240  
Db 3181 CGTATGCTGCTCCAGGAGCAACATCCGAGCAGACCCAGACGAAATGGGTCCAGCAAAAG 3240  
QY 3241 CCGACTACATGCTGAAACAAAGGTGAGAAATCCCGGAGCAGAGACCCATGAGATGCCC 3300  
Db 3241 CCGACTACATGCTGAAACAAAGGTGAGAAATCCCGGAGCAGAGACCCATGAGATGCCC 3300  
QY 3301 AGTTCCCTTTCTACCTTCAACGAGGCTTGAGGAGACACCTCAGACTTTGTGAGAGCAATTGAAA 3360  
Db 3301 AGTTCCCTTTCTACCTTCAACGAGGCTTGAGGAGACACCTCAGACTTTGTGAGAGCAATTGAAA 3360  
QY 3361 AAGTAAGACCATCTGAGCAACTATACGAGCCCTGGGGCTGTCCAGTTAACCCCAAGGCT 3420  
Db 3361 AAGTAAGACCATCTGAGCAACTATACGAGCCCTGGGGCTGTCCAGTTAACCCCAAGGCT 3420  
QY 3421 ACCCTTCTCTTCTGAGGAGCAGTACATCGGCTCCGCAATGGCTGCTGTGATCA 3480  
Db 3421 ACCCTTCTCTTCTGAGGAGCAGTACATCGGCTCCGCAATGGCTGCTGTGATCA 3480  
QY 3481 GCGTGTGTGAGCTGACATTCCTGCTGAGCCTGCTCTTCTGAAACCCCTGAGAGG 3540  
Db 3481 GCGTGTGTGAGCTGACATTCCTGCTGAGCCTGCTCTTCTGAAACCCCTGAGAGG 3540  
QY 3541 CCGGAGATCATTTGATGCTCTGAGGCTGATGAGCGTGAAGCTGTTGGCATATGAGGCC 3600  
Db 3541 CCGGAGATCATTTGATGCTCTGAGGCTGATGAGCGTGAAGCTGTTGGCATATGAGGCC 3600  
QY 3601 TCATGGAATCAAGCTAGTGCCTGAGCCGCTGAGTCACTGATGCTGTGAGCATAG 3660  
Db 3601 TCATGGAATCAAGCTAGTGCCTGAGCCGCTGAGTCACTGATGCTGTGAGCATAG 3660  
QY 3661 GAGTGAAGTTACACCTTACAGTTGCTTGGCTTCTGACGAGCCATCGGCGCAAGAAAGC 3720  
Db 3661 GAGTGAAGTTACACCTTACAGTTGCTTGGCTTCTGACGAGCCATCGGCGCAAGAAAGC 3720  
QY 3721 GCAAGGCTGTGCTTGGCTTGGAGCAGCATGTTTGCACCCGCTCTGATGAGCCGCTGCTCA 3780  
Db 3721 GCAAGGCTGTGCTTGGCTTGGAGCAGCATGTTTGCACCCGCTCTGATGAGCCGCTGCTCA 3780  
QY 3781 CTCTGCTGGAGAGTCTGATGCTGAGGAGATGAGTTGACATTCATGTCAGATTTTCT 3840  
Db 3781 CTCTGCTGGAGAGTCTGATGCTGAGGAGATGAGTTGACATTCATGTCAGATTTTCT 3840  
QY 3841 TTGCTGTGCTGAGCATCTCAGCATCTCGGCTTCTCAATGAGGCTGCTTTCCTCCG 3900  
Db 3841 TTGCTGTGCTGAGCATCTCAGCATCTCGGCTTCTCAATGAGGCTGCTTTCCTCCG 3900  
QY 3901 TGCCTTTTGTCTTCTTGGACCATATCTGAGAGTGTCTCCAGCCAGCCGCTTGAACCCGC 3960  
Db 3901 TGCCTTTTGTCTTCTTGGACCATATCTGAGAGTGTCTCCAGCCAGCCGCTTGAACCCGC 3960  
QY 3961 TGCCCAACACCTGCTGAGCAGCCCGCAGCGGCTGCGCTGCAATGCGCCAGCCGC 4020  
Db 3961 TGCCCAACACCTGCTGAGCAGCCCGCAGCGGCTGCGCTGCAATGCGCCAGCCGC 4020  
QY 4021 ACAAGCAGAGGCTGATTCCTCCGACTCGGAGATATGATTTCCAGAGCAGAGTGTAG 4080  
Db 4021 ACAAGCAGAGGCTGATTCCTCCGACTCGGAGATATGATTTCCAGAGCAGAGTGTAG 4080  
QY 4081 GCTCTACGAGAGGCTTGGCAGTACGAGGCGCAGAGGCGCGGAGGCTTGCACAC 4140  
Db 4081 GCTCTACGAGAGGCTTGGCAGTACGAGGCGCAGAGGCGCGGAGGCTTGCACAC 4140  
QY 4141 AAGTGAATCGTGAAGCCAGAAACCCGCTTCTGAGCAGCTCCACATGCTGCTCAATCCG 4200  
Db 4141 AAGTGAATCGTGAAGCCAGAAACCCGCTTCTGAGCAGCTCCACATGCTGCTCAATCCG 4200



[illegible]

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QY	1501	ACGAGACATTCGAAGGGGTACGAGATATGTCTCACACATCAACTGTGAACGAGACAAACGCG	1566
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QY	1561	CAGCCATCTCGAGGECCTGGCAGAGAGACATATGTGAGAGTGGTTTCATCAGAGTGTGCGAC	1620
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Db	1681	CGTTCCTCAGCGTCAGTGTGCATCCGGGTGGCCAGCGGCTACTTACTCATGTGCGCTATG	1740
QY	1741	CGTGTTCACCATGCTGCGGTGGAGCTGCTCCAAAGTCCAGAGGTGCCGTGGGGCTGGCGTG	1800
Db	1741	CGTGTTCACCATGCTGCGGTGGAGCTGCTCCAAAGTCCAGAGGTGCCGTGGGGCTGGCGTG	1800
QY	1801	GGGTCTGCTGCTGGTTGTCACCTGTCAGTGGCTGACAGACTGGGCGCTGTCTCATTTGACGAA	1866
Db	1801	GGGTCTGCTGCTGGTTGTCACCTGTCAGTGGCTGACAGACTGGGCGCTGTCTCATTTGACGAA	1866
QY	1861	TTTCCCTTAAAGGTGGAACAAACACAGGTTTGGCATTTTCGCGCTGGGTGGTGGTGGG	1920
Db	1861	TTTCCCTTAAAGGTGGAACAAACACAGGTTTGGCATTTTCGCGCTGGGTGGTGGTGGG	1920
QY	1921	ATGATGTTTTTTTCTTCTGCGCCACAGCCTTCAGTGAACAGAGACAGAAATAAAGATCCCTT	1988
Db	1921	ATGATGTTTTTTTCTTCTGCGCCACAGCCTTCAGTGAACAGAGACAGAAATAAAGATCCCTT	1988
QY	1981	TTGAGACACAGGACCGGGGAGTGGCTTGAAGCGCACAGAGACCGACGCTGGCCCTCACGTTCA	2040
Db	1981	TTGAGACACAGGACCGGGGAGTGGCTTGAAGCGCACAGAGACCGACGCTGGCCCTCACGTTCA	2040
QY	2041	TCAGCAATGTGCAAGGCTTCTTCATGGCGCGGTTAAATCCCAATTCGCCGCTGTGGGGGGGT	2100
Db	2041	TCAGCAATGTGCAAGGCTTCTTCATGGCGCGGTTAAATCCCAATTCGCCGCTGTGGGGGGGT	2100
QY	2101	TCCTCCCTCAGGACGGCGTATGATGGTGTTCATATTTTGGCATGGTTCTGCTCATTTTTC	2166
Db	2101	TCCTCCCTCAGGACGGCGTATGATGGTGTTCATATTTTGGCATGGTTCTGCTCATTTTTC	2166
QY	2161	CTGCAATTCCTCAGCATGAGATTTATTCAGCGCGGACAGAGAGACTGGATTTTCTTGCT	2220
Db	2161	CTGCAATTCCTCAGCATGAGATTTATTCAGCGCGGACAGAGAGACTGGATTTTCTTGCT	2220
QY	2221	GTTTTTCAAGCCCTCGTCGTCAGAGAGTGAATTCAGGTTGAACCTCAGGCGCTACACCGACA	2280
Db	2221	GTTTTTCAAGCCCTCGTCGTCAGAGAGTGAATTCAGGTTGAACCTCAGGCGCTACACCGACA	2280
QY	2281	CACACAGACATACCCGCTACAGCGCCCCCACCCTCCCTACACAGCGCACAGCTTTCGCATG	2340
Db	2281	CACACAGACATACCCGCTACAGCGCCCCCACCCTCCCTACACAGCGCACAGCTTTCGCATG	2340
QY	2341	AAACGAGATTACCATGACATCCACTGTCCAGCTCCGCGACGAGTACGACCCCGACACGC	2400
Db	2341	AAACGAGATTACCATGACATCCACTGTCCAGCTCCGCGACGAGTACGACCCCGACACGC	2400
QY	2401	ACGTGTACTACACACACCGCTGACCGCGGCTCCAGAGATCTGTGTACACCGCTCACCGTGA	2466
Db	2401	ACGTGTACTACACACACCGCTGACCGCGGCTCCAGAGATCTGTGTACACCGCTCACCGTGA	2466
QY	2461	CACAGACACACCTCAGCTGTGCAAGCGCCACAAGAGACACACACTCCACAAAGGAGACTGTCT	2520
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Qy 2581 CATCTTTGCTGAGAACACTATCTCTTCTCTGTAACCAAAAGCAAGGTAGTG 2640
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Qy 2821 CGAATATCCAGACTTACTTACGACCTTACACAGAGATTTCAGTAACTGAGATATGCA 2880
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QY 5281 CCGGAATT 5288
DB 5281 CCGGAATT 5288

```

# RESULT 4

US-08-857-636-1  
Sequence 1, Application US/08857636

## GENERAL INFORMATION:

APPLICANT: Dean, Michael Carlton  
APPLICANT: Hahn, Heidi Eve  
APPLICANT: Wickling, Carol  
APPLICANT: Christiansen, Jeffrey  
APPLICANT: Zaphiropoulos, Peter G.  
APPLICANT: Gallant, Mae R.  
APPLICANT: Shanley, Susan Mary  
APPLICANT: Chidambaram, Adirami  
APPLICANT: Vorechovsky, Igor  
APPLICANT: Holmberg-Lindstrom, Erika  
APPLICANT: Unden, Anne Birgitte  
APPLICANT: Gillies, Susan Alana  
APPLICANT: Negus, Kylie  
APPLICANT: Smyth, Ian Mcleod  
APPLICANT: Pressman, Carol Leah  
APPLICANT: Lefell, David J.  
APPLICANT: Gerard, Bernard  
APPLICANT: Goldstein, Alisa Miriam  
APPLICANT: Mainwright, Brandon  
APPLICANT: Totfgard, Rune Carl-Wagnus  
APPLICANT: Chenevix-Trench, Georgia  
APPLICANT: Bale, Allen E.  
TITLE OF INVENTION: A Basal Cell Carcinoma Tumor Suppressor Gene  
NUMBER OF SEQUENCES: 83  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor

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? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/857,636
? FILING DATE: 16-MAY-1997
? CLASSIFICATION: 514
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/017,906
? FILING DATE: 17-MAY-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: AU P00011
? FILING DATE: 21-MAY-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: AU P00363
? FILING DATE: 07-JUN-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/019,765
? FILING DATE: 14-JUN-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Hunter, Tom
? REGISTRATION NUMBER: 38,498
? REFERENCE/DOCKET NUMBER: 015280-27820005
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 1:
? LENGTH: 6568 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: -
? LOCATION: 1..6568
? OTHER INFORMATION: /note= "human nevold basal cell
? OTHER INFORMATION: carcinoma syndrome (NBCCS)
? OTHER INFORMATION: (PATCHED (PTC)) cDNA"
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 442..4332
? US-08-857-636-1

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Query Match 88.6%; Score 4684.8; DB 12; Length 6568;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 4692; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 585 GGAAGAGCTACTGCGCGAAGAGCCCACTGCGCTGAGAGGGAAGTTTCAAGACTCTT 644
DB 190 GGAAGAGCTACTGCGCGAAGAGCCCGCTGCGCTGAGAGGGAAGTTTCAAGACTCTT 644
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DB 250 TTTAACTGGGTGTTCAATTTCAAAAAAAGTGGGCAAGTTCTTGGTTGGGCTCTCTC 704
QY 705 ATATTTGGGCGCTTGGGCGTGGGATTTAAAGCAGCAAGCTCGAGACCAAGTGAGAG 764
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QY 765 CTGAGCTGAAGTTGAGAGCAGAGTAAGCTGAATTAATTAATTAATTAATTAATTAAT 824
DB 370 CTGAGCTGAAGTTGAGAGCAGAGTAAGCTGAATTAATTAATTAATTAATTAATTAAT 824
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Db 430 GGAGAAAGAGGCTATGTTAACTCTCAACTCATGATACAGACCCCTAAAGAAAGAGGTGCT 489  
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Db 2410 CAGAAAGCAGACTACCGGAATATCAGCACTTACTTACGACTTACTTACAGAGAGTTCACT 2469  
Qy 2865 AACGTGAATGTATCATGTTTGAAGAAACAAACAGCTTCCCAAAATGTGCTGCACTAC 2924  
Db 2470 AACGTGAATGTATCATGTTTGAAGAAACAAACAGCTTCCCAAAATGTGCTGCACTAC 2529  
Qy 2925 TTCAGAGACTGCGTTCAGGAGCTTCAAGATGCAATTTGACATGATGAGGAAACCGGAAA 2984  
Db 2530 TTCAGAGACTGCGTTCAGGAGCTTCAAGATGCAATTTGACATGATGAGGAAACCGGAAA 2589  
Qy 2985 ATCATGCCAAACATTTCAAGAAATGATCAGACGATGAGTCTTCTCTACAACTCTGT 3044  
Db 2590 ATCATGCCAAACATTTCAAGAAATGATCAGACGATGAGTCTTCTCTACAACTCTGT 2649

QY 3045 GTGCAACCGGCGAGCGGATGATGAGCCATGACATCAGCCAGTGTACTAAACAGCGTCTG 3104  
DB 2650 GTGCAAAACCGGCGAGCGGATGATGAGCCATGACATCAGCCAGTGTACTAAACAGCGTCTG 2709  
QY 3105 GTGATGACAGATGGATCATTTAAATCCAGGCGTTTCTACATCTCTACCTGACGGCTTTGGGTC 3164  
DB 2710 GTGATGACAGATGGATCATTTAAATCCAGGCGTTTCTACATCTCTACCTGACGGCTTTGGGTC 2769  
QY 3165 AGCAAGACCGCGTCCGCTATGCTCCAGGCGCAACATCCGGCGACACGACGACGAA 3224  
DB 2770 AGCAAGACCGCGTCCGCTATGCTCCAGGCGCAACATCCGGCGACACGACGACGAA 2829  
QY 3225 TGGGTCACAGACAAGCCGATCAGCTGAAACAGAGGCTGAGATCCGGCAGCAGAG 3284  
DB 2830 TGGGTCACAGACAAGCCGATCAGCTGAAACAGAGGCTGAGATCCGGCAGCAGAG 2889  
QY 3285 CCCATGAGATGATCCGATGCTTCTACCTCAAGGGGTTGGCGGACACTCAGACTTT 3344  
DB 2890 CCCATGAGATGATCCGATGCTTCTACCTCAAGGGGTTGGCGGACACTCAGACTTT 2949  
QY 3345 GTGAGAGCAATTTGAAAAAGTAAGACCATCTGACAGCAACTATACGAGCGTGGGCTGTCC 3404  
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QY 3525 CTGACCCCTTGAAGCGGCGGATCATTTGATGATGCTGCTGCGCTGATGAGCGTGCAGCTG 3584  
DB 3130 CTGACCCCTTGAAGCGGCGGATCATTTGATGATGCTGCTGCGCTGATGAGCGTGCAGCTG 3189  
QY 3585 TTGGGATGATGGGCTCATGTCGAAATCAGCTCAGTGCCTGCGCTGCTGCTGCTGCTGCTG 3644  
DB 3190 TTGGGATGATGGGCTCATGTCGAAATCAGCTCAGTGCCTGCGCTGCTGCTGCTGCTGCTG 3249  
QY 3645 GCTTCTGTTGGATAGAGATGAGTTCACCGTTTACGTTTGGGCTTTCGAGGCGC 3704  
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QY 3765 GATGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3824  
DB 3370 GATGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3429  
QY 3825 ATTGTCAGATATTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3884  
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QY 3945 AACGCGTTGAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4004  
DB 3550 AACGCGTTGAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3609  
QY 4005 GCCATGCGCGCGGCGCACAGCAGCGGCTGATCTCTGCGACTCGGAGTATGATTC 4064  
DB 3610 GCCATGCGCGCGGCGCACAGCAGCGGCTGATCTCTGCGACTCGGAGTATGATTC 3669  
QY 4065 CAGAGCAAGTGTCAAGGCTCAGCGAGAGCTTGGCGACTACGAGGCGCCAGCGGCGG 4124  
DB 3670 CAGAGCAAGTGTCAAGGCTCAGCGAGAGCTTGGCGACTACGAGGCGCCAGCGGCGG 3729  
QY 4125 GGAGGCGCTGCGCACCAAGTGTATGTGAGGCGCACAGAAACCGCTTCTTCCGCCACTCC 4184

DB 3730 GGAGGCGCTGCGCACCAAGTGTATGTGAGAGCCACAGAAACCGCTTCTTCCGCCACTCC 3789  
QY 4185 ACTGTCTTCATCCCGAATCCAGGATCAACCCACCTCGAACCAGAGACAGACGCCCCAC 4244  
DB 3790 ACTGTGTCTCATCCCGAATCCAGGATCAACCCACCTCGAACCAGAGACAGGCCCCAC 3849  
QY 4245 CTGAGCTCAGGAGTCCCTGCTCCCGGACGAGGCGCAGAGGCTCCGCGAGGACCCCCC 4304  
DB 3850 CTGAGCTCAGGAGTCCCTGCTCCCGGACGAGGCGCAGAGGCTCCGCGAGGACCCCCC 3909  
QY 4305 AGAGAAAGCTTGTGGCACCCCTCTACAGACCGCGAGAGAGCTTTTGAATTTTACT 4364  
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QY 4365 GAAGGCGATTTGTGGCCCTAGCAATAGAGGCGCGTGGGCGCTTCCGCGGCGGCTTCTAC 4424  
DB 3970 GAAGGCGATTTGTGGCCCTAGCAATAGAGGCGCGTGGGCGCTTCCGCGGCGGCTTCTAC 4029  
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DB 4030 AACCTCGGAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4089  
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DB 4150 GGGCGTGGGCGGAACCCCGGAGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4209  
QY 4605 CTGTTTGAAGAGACCCCGAGGCTTCTCCACGCTCCGCTGAGAGGAGGATTCGAAAGG 4664  
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DB 4510 TTAAGAGATGTAACAGTGTGTAATATTAAGAGAGAGATGTAATGATGATATCTGGG 4569  
QY 4965 CTTCACACTCTGCGCCAGAGTGTGAGGCGCACAGTGGGCGCTCTCGATTTGTGAT 5024  
DB 4570 CTTCACACTCTGCGCCAGAGTGTGAGGCGCACAGTGGGCGCTCTCGATTTGTGAT 4629  
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DB 4630 TGGGCTCGGTCGACAGCAACAGCTTCAATTAATTTTCAAGATATGTTGCTGCTG 4689  
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DB 4690 TTAATATTTGTAATTTTACTGTAATTTTCAAGCAATATTTGCTTGTGTAATAGAT 4749  
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DB 4750 ATTTTGAAGGTTCTGTTTAAATATTTTAAATTTGCAATATACACCTGTGTGT 4809  
QY 5205 ATGAATGTTACTGTTTAACTTCAACAGCTATGCTGATTAATTTTGTAAATGAG 5264







Db	3657	1CCAA6T6TCGTCGGTTT6CCGTGCTTCGT6GTCAACGAACAAATGG6GTGATTTCTC	3718
QY	4046	GCACTCGAGATATAGTATCTCCACAGACAGAGTGTCAAG6CCTCAAGCGAGAGCTTCGGCACTA	4105
Db	3717	GCACTCGAGATACACCTCTCCAGACACAGCTGTGTCATGTAGAGAGCTCAGCAATA	3776
QY	4106	CGAGGCGCCGAGAGGGGCGGGGAGGCGCTT6CCACCAGTATGTGTGGAAGCCACAGAAAA	4165
Db	3777	CGAACACAGCAGG6GTGTGCGGAGAGGCGCTTCCACCAAGTGTGTGTGGAAGCCACAGAAAA	3836
QY	4166	CCCCGCTTTCGCCACCTCTCACTGTGTGTTCATATCCGAATCCAGGATATACCCACCTCGAA	4225
Db	3837	CCGTGTCTTTCGCCGGGTCCACTGTGTGTGTCAATCCGAGACTCCAGATATACGCTTCCCTTGC	3896
QY	4226	CCCGAGACAGACAGCCCCACCTGAGACTAGAGGTCCCTGCTCCCTCCGAGCGGACAGGCCAGCA	4285
Db	3897	CCCTGTGGAAAGAGCCCCACCTGAGACTGTGGCTCTTGTCTCCCTGTGAGCGGCAAGGCCAGCA	3956
QY	4286	GCCCCGCGAGGAGACCCGCCACAGAGAAGGCTTGTGGCCACCCCTCTACAGACCGCGCACAGA	4345
Db	3957	GCCTCGAAGGAGATCCCTCTAGAGAAGCTTGTGGCCACACCCCTACAGACCGGCCACAGA	4016
QY	4346	CGCTTTTGAATTTTCTACTGTAGAGGCAATTGTGGCCCTAGCAATAGGGCCCGCTGGGGCCC	4405
Db	4017	CGCTTTTGAATTTTCTACTGTAGAGGCAATTTGTGGCCCTAGCAATAGGAGCGCTCAGGGCC	4076
QY	4406	TCGCGGGGGCCGTTCTCAACAACCTCGGAACCCAGCGTCCACATGCCATGGGCGAGCTCCGT	4465
Db	4077	CCGTGGGGCCCGTTCTCAACAACCTCGGAACCCAGCGTCCACATGCCAGTGGCGCTCTGT	4136
QY	4466	GCCCCGCTACTGCCAGCCCATCAACACTGTGTAGCGGCTTGTGCCCTCGTGTGATGTGCGCGT	4525
Db	4137	GCCCCGCTACTGCCAGCCCATCAACACTGTGTAGCGGCTTGTGCTCGGTGATGTGTCTGT	4196
QY	4526	GCAACCCGCGCTGTCCCTGGGCGTGGGCGGGAACCCCGAGGGGGGACTGTGCCAG-----	4581
Db	4197	GCATCCCCCG-----CCTGAGACTGTGGCGCAACCCCGAGGGGGGCGCTGTCCAGGCTA	4250
QY	4582	-----GCTACCCGTGAGACTGACCAAGCGCTGTTTGAAGAACCCCGACGCTGTTCACGCT	4636
Db	4251	TGAGAGCTACCCGTGAGACTGATACAGGGGATTTTGAAGATCTCATGTGCTTTTCATGT	4310
QY	4637	CCGCTGTGAGAGAGGAGGATTCGAAGGTGGGAAGTCATTGAGCTGCAGAGAGTGGATGCCA	4696
Db	4311	CAGGTGTGAGAGAGGAGGACTCAAAAGTGTGGGTCATAGAGCTACAGAGCTGGAAATCTGA	4370
QY	4697	GGAGAGCCCCCGGGGAGAGCAAGCTCCAACTGAGGGTGATTTAAATCTGAAGCAAAAGAGGCC	4756
Db	4371	GGAGAGGCCGCTGGGGGAGAGCAAGCTCCAACTGAGGGTATTTAAATCTGAAGCAAAAGAGGCC	4430
QY	4757	AAAGATTTGGAAACCCCCCACCACCCCAACCTCTTTCAGAACTGCTTGAAGAGAACTGGTTGG	4816
Db	4431	AAAGATTTGGAAA-----GCCCCCGCCCCCAACCTCTTTCAGAACTGCTTGAAGAGAACTGGTTGG	4489
QY	4817	ACTTATGAAAAAGATGCCCCGTGTGCCAGACAGCAAGTCTTATTTACTGTAAACGATTTGA	4876
Db	4490	AATTTATG-----GGAAGGCAAGTCAATTTTACTGTAACTGATTTGTA	4530
QY	4877	TATATTTTGTAAATATTTTCTATATTAATTTTAAGACATGTACAGATGTAAATATAGAG	4936
Db	4531	TATATTTTGTAAATATTTTCTATATTAATTTTAAGAGTGTACACA-----TGTAAATATACATGG	4588
QY	4937	GAGGATGTAAAGTGTATGTATCTGGGGCTTCTCACATCTCGGCCACAGAGTGTGAGAGGCC	4996
Db	4589	AAATCTGTACAGT-----CTATTTCCTTGGGGCTCTCCACATCTCGGCCACAGAGTGTGAGAGGCC	4647
QY	4997	ACAGTGGGGGCGCTCCGATTTGTGTCATTGGGCTCGGTGCCACAACAAGCTTATTAGT	5056
Db	4648	ACA-----GGGGCCCTTTCCTGTGTACATTTGGTCTCTGTGCCACAACAAGCTTAACTTAG	4705
QY	5057	CTTAAA-----TTTCAGATATGTGTGTGCGCTTAAATATTTGTATTTACTTGT	5108
Db	4706	TTTTAAAAAAATCTCCAGCATATGTGTGCTGTCTTAAATATTTGTATTTACTTGT	4765

QY	5109	ATATTTCTATGCAAAATTTCTCTATATGTAATAGATTATTTGTAAAGCTTCTGTTTAA	5168
Db	4766	ATAATTTCTATGCAAAATTTCTCTATATGTAATAGATTATTTGTAAAGCTTCTGTTTAA	4824
QY	5169	ATATTTAAATTTGCATATACAAACCTGTGGTAGTATAGTAATGTACTGTTAACTTCA	5228
Db	4825	ATATTTAAATTTGCATATACAAACCTGTGGTAGTATAGTAATGTACTGTTAACTTTC	4884
QY	5229	AACACGCTATGCGTATATTTTTTTGTTTAAAGACAGATATGAAGAAGC	5280
Db	4885	AACACGCTATGCGTATATTTTTTTGTTTAAAGACAGATATGAAGAAGC	4931

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1      RESULT      6
2      US-08-954-655-9
3      ; Sequence 9, Application US/08954655
4      ; GENERAL INFORMATION:
5      ; APPLICANT: SCOTT, MATHEW P
6      ; JOHNSON, RONALD L
7      ; GOODRICH, LISA V
8      ; TITLE OF INVENTION: Patched Genes and their use
9      ; NUMBER OF SEQUENCES: 19
10     ; CORRESPONDENCE ADDRESS:
11     ; ADDRESSEE: Foley, Hoag & Eliot
12     ; STREET: One Post office Square
13     ; CITY: Boston
14     ; STATE: MA
15     ; COUNTRY: USA
16     ; ZIP: 02109
17     ; COMPUTER READABLE FORM:
18     ; MEDIUM TYPE: floppy disk
19     ; COMPUTER: IBM PC compatible
20     ; OPERATING SYSTEM: PC-DOS/MS-DOS
21     ; SOFTWARE: ASCII(text)
22     ; CURRENT APPLICATION DATA:
23     ; APPLICATION NUMBER: US/08/954,655
24     ; FILING DATE: 20-Oct-1997
25     ; CLASSIFICATION: <unknown>
26     ; ATTORNEY/AGENT INFORMATION:
27     ; NAME: Vincent, Matthew P.
28     ; REGISTRATION NUMBER: 36709
29     ; REFERENCE/DOCKET NUMBER: SUV-003.06
30     ; TELECOMMUNICATION INFORMATION:
31     ; TELEPHONE: 617-832-1000
32     ; TELEFAX: 617-832-7000
33     ; INFORMATION FOR SEQ ID NO: 9:
34     ; SEQUENCE CHARACTERISTICS:
35     ; LENGTH: 5187 base pairs
36     ; TYPE: nucleic acid
37     ; STRANDEDNESS: single
38     ; TOPOLOGY: linear
39     ; MOLECULE TYPE: cDNA
40     ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
41     US-08-954-655-9

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Query Match	71.9%;	Score 3801.2;	DB 13;	Length 5187;
Best Local Similarity	88.1%;	Pred. No. 0;		
Matches 4276;	Conservative	3;	Mismatches 516;	Indels 57;
			Gaps	11
QY 446	CGGTGCCCCCGGAGCGCCCGCTGTGTAGAGCGCGAGGCGCAGACGGAGCGGGGGGCTGTGGCGG			505
Db 120	CGGGGCGCCCTGTGTGACAGGCGCGGGCGGGAGGGCCCAACAGCAGCCGGGGAGCCGACCGG			179
QY 506	TGCTGCGCGCGCGGAGGAGTATCTGTGACCGCGCCCACTACTGTGAGCGCCGCTTCGC			565
Db 180	C----GCGGCGCGGACCGGAGTATCTGTGACCGCGCCCACTACTGTGAGCGCCGCTTCGC			236
QY 566	TCTGTGAGCAGATTTTCCAAAGGGGAAAGGCTACTGGCGGAAAGGCGCACTGTGGCTATAGAGC			625
Db 237	TCTGTGAGCAGATTTTCCAAAGGGGAAAGGCTACTGGCGGAAAGGCGCGCTGTGGCTATAGAGC			296



Db 2457 CAACATGTATATAGTCACCCGAAAGACACTACCCGAAATTCACAGCACTACTTACGA 2516  
QY 2846 CCTACACAGAGATTTCAGTAACGTAGATATGTATGTGAGAAACAAACAGCTTCC 2905  
Db 2517 CCTCATTAAGAGTTTCACACATGTGAATGTCTATGCGGAGGAGAACACAGCACTTCC 2576  
QY 2906 CAANAATGGGCTGCACCTACTTCAGAGACTGGCTTCAGGAGCTTCAGATGCAATTTGACAG 2965  
Db 2577 CCAATATGGGCTGCACCTACTTCAGAGACTGGCTTCAGGAGCTTCAGATGCAATTTGACAG 2636  
QY 2966 TGACTGGGAAACCGGAGAAATCATGCGCAAAACATTCACAAGATGATCGACAGATGAGAT 3025  
Db 2637 TGACTGGGAAACCTGGAGAGATCATGCCAACATTTATAAAATGGATTCAGATGACGGGCT 2696  
QY 3026 CATTGCTTACAACTCCTGTGTGCAAAACCGGAGCGCGATAGACCATAGCATGACGCCA 3085  
Db 2697 CTTGCTTACAACTCCTGTGTGAGACTGGCAGCGGAGACAAAGCCCATGACATTAAGTGA 2756  
QY 3086 GTTGAATTAACAGGCTGTGGTGGATGCGAGATGGCATCTAATTAATCCAGCGCTTTCACAT 3145  
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QY 3146 CTACCTACAGGCTTGGGTGACAGCAAGCCCGTGCATGTGCTGCTCCAGGCGCAACAT 3205  
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QY 3326 GCGGAGACACTCAGACTTGTGAGGCAATGAAAAAGTAAAGACATCTGACAGACAT 3385  
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QY 3446 CATGAGCTTCCGACACAGCTGCTGCTGTCATCAGGCTGGTGTGGCTGCTGACATTCCT 3505  
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QY 3746 CATGTTGACCGGCTGCTGGATGGGCGGCTGTCACATCTGCTGGAGATGGCTGATGCTGGC 3805  
Db 3417 CATGTTGCTCCGCTTGTGAGCGGTGTGTGCTCAGCTCTCTGGTGTACTGATGCTTGC 3476  
QY 3806 GGGATTCGATTCGATTCATGTCAGATATTTCTTGTGCTGTGCGATGCGATTCACACAT 3865  
Db 3477 AGGGTCGGAATTTGATTCATGTCAGATATCTTGTGGCGTCTCGGCAATTCACACAT 3536  
QY 3866 CCGGCGGCTTCAATGAGGCTGTGTGCTTCCGCTTGTGTGCTTGTGCTTGTGAGCATA 3925  
Db 3537 CTTGGGGGCTTCAATGAGGCTGTGTGCTTCCCTGCTGCTGCTTATCTTGTGAGCGCTG 3596

QY 3926 TCCGTGAGGTGTCTCAGCAACGCGCTTGAACCGCTTGCACACCGCTCCCTGAGCCACC 3985  
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QY 4226 CCGGAGACAGACCGCCACCTGAGTGAAGGCTCCCTGCTCCGAGCGCAAGCCAGCA 4285  
Db 3897 CCGTGGGCAACAGCCCGACCTGAGCTGTGGCTCTTGTGCTGCGGAGGCGAGGCGACCA 3956  
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Db 3957 GCGTCCAGAGGATCCCGCTGAGAAAGGCTTGGCGCCACCGCTTACAGACCGCGAGAGA 4016  
QY 4346 CCGTGTGAAATTTCTACTGAAGGCGATCTGGCGCTTGAAGATGAGGCGCGCGGCGCC 4405  
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QY 4406 TCGGCGGCGCGCTTCTCACAACCTCGGAACCCAGCGTCCATGCGATGCGGACCTCGT 4465  
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QY 4466 GCGCGGCTACTGCGACCGCATCACAACCTGATGAGGCGCTTGGCGCTGCGTGTGCGCGCT 4525  
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QY 4697 GGAAGGCGCGCGGAGAGGAGCTCAACTGTAGGCTGATTTAAATTCGAAACCAAGAGGCC 4756  
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QY 1646 CTTCCACCAACGACGACCTTGAGACATTCCTGAATCCTTCTGTGACGTGATGATCCG 1705  
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 QY 1886 GGTGACAGGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1945  
 Db 1557 GGTGACAGGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1616  
 QY 1946 CTTGAGTGAACAGGACGAGATTAAGATCCCTTTTGAGAGACGAGACGCGGAGTGCCT 2005  
 Db 1617 ATTGAGTGAACAGGACGAGATTAAGATCCCTTTTGAGAGACGAGACGCGGAGTGCCT 1676  
 QY 2006 GAAGCCACAGGAGGACGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2065  
 Db 1677 GAAGCCACAGGAGGACGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1736  
 QY 2066 GGTGACAGGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2125  
 Db 1737 GGTGACAGGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1796  
 QY 2126 GGTGACAGGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185  
 Db 1797 GGTGACAGGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856  
 QY 2186 TGGAGCGGAGGACGAGATGATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2245  
 Db 1857 TGGAGCGGAGGACGAGATGATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1916  
 QY 2246 AGTGAATGAGTGAACCTGACGCTGACGACGACGACGACGACGACGACGACGACGAC 2305  
 Db 1917 GGTGATGACGTTGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 1976  
 QY 2306 CCCACCTCCCTACAGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2365  
 Db 1977 CCCACCTCCCTACAGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2036  
 QY 2366 TGTGACGCTCCGAGGAGTACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2425  
 Db 2037 TGTGACGCTCCGAGGAGTACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2096  
 QY 2426 GGTGACGCTCCGAGGAGTACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2485  
 Db 2097 AGCTGCTGAGTCTCTGTAAGGCTGTTACGCTGACCCAGGACGACGACGACGACGACGAC 2156  
 QY 2486 CCCAAGAGACGACGACGCTCCACAGGAGACGCTGCTCCGAGTCTCCGAGTCTCCGAG 2545  
 Db 2157 TCCCAAGAGACGACGACGCTCCACAGGAGACGCTGCTCCGAGTCTCCGAGTCTCCGAG 2216  
 QY 2546 CTGCTGAGGACGCTCCGAGGAGTACGACGACGACGACGACGACGACGACGACGACGAC 2605  
 Db 2217 CTGCTGAGGACGCTCCGAGGAGTACGACGACGACGACGACGACGACGACGACGACGAC 2276  
 QY 2606 TCTGTTCTCTTGAACCAAAAGGCTAGTGTGATCTTCTGTTCTGTTCTGTTCTGTTCTG 2665  
 Db 2277 TCTGTTCTCTTGAACCAAAAGGCTAGTGTGATCTTCTGTTCTGTTCTGTTCTGTTCTG 2336  
 QY 2666 GGGGGTCAAGCTTTATGAGACGACGAGATGAGAGAGAGGCTGAGACCTTACGAGACATGT 2725  
 Db 2337 GGGGGTCAAGCTTTATGAGACGACGAGATGAGAGAGAGGCTGAGACCTTACGAGACATGT 2396

QY 2726 ACCTGGGAACGAGAGATATGACTTATTTGCTGACAAATTCAAATCTTTCTTTCTA 2785  
 Db 2397 TCCCGGGAAACGAGAAATATGACTTATTTGCTGACAAATCTTTCTTTCTA 2456  
 QY 2786 CAACATGATATATGATACCCAGAAAGGAGACTACCCGAAATATCCAGAGCTTACTTACA 2845  
 Db 2457 CAACATGATATATGATACCCAGAAAGGAGACTACCCGAAATATCCAGAGCTTACTTACA 2516  
 QY 2846 CCTACAGAGAGTTTCAGTACGATGAAGTATGTCATGTTGGAAGAAACAAACAGCTTTC 2905  
 Db 2517 CCTACAGAGAGTTTCAGTACGATGAAGTATGTCATGTTGGAAGAAACAAACAGCTTTC 2576  
 QY 2906 CAAATGAGGCTGACACTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2965  
 Db 2577 CAAATGAGGCTGACACTTCCAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2636  
 QY 2966 TCACTGGGAACCGGAAATCATGACCAAAATTAACAAAGATGACAGCTGAGT 3025  
 Db 2637 TCACTGGGAACCGGAGAGATCATGACCAAAATTAACAAAGATGACAGCTGAGT 2696  
 QY 3026 CTTGCTGCTCAAACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3085  
 Db 2697 CTTGCTGCTCAAACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2756  
 QY 3086 GTTGACTAAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3145  
 Db 2757 GTTGACTAAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2816  
 QY 3146 CTACCTGACGCGTTGGGTGACGACGACGACGACGACGACGACGACGACGACGACGAC 3205  
 Db 2817 CTACCTGACGCGTTGGGTGACGACGACGACGACGACGACGACGACGACGACGACGAC 2876  
 QY 3206 CCGGACACGACGAGAGATGGGTCCACGACAAAGCCGACTACATGCTGTAACAAAGCT 3265  
 Db 2877 CCGGACACGACGAGAGATGGGTCCACGACAAAGCCGACTACATGCTGTAACAAAGCT 2936  
 QY 3266 GAGAAATCCCGGACGAGAGCCCATGAGTATGCGCAGTTCCCTTCTACCTCAAGGGTT 3325  
 Db 2937 GAGAAATCCCGGACGAGAGCCCATGAGTATGCGCAGTTCCCTTCTACCTCAAGGGTT 2996  
 QY 3326 GCGGACACCTGAGACTTTGTGAGAGCAATGTAAGAAAGTAAGGACCATGTCAGCACTA 3385  
 Db 2997 GCGGACACCTGAGACTTTGTGAGAGCAATGTAAGAAAGTAAGGACCATGTCAGCACTA 3056  
 QY 3386 TAAGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3445  
 Db 3057 TAAGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3116  
 QY 3446 CATCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3505  
 Db 3117 CATCGGCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3176  
 QY 3506 CGTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3565  
 Db 3177 AGTGTGCGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3236  
 QY 3566 GCTGATGACGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3625  
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 QY 3626 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3685  
 Db 3297 GCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3356  
 QY 3686 TTTGGGCTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3745  
 Db 3357 TTTGGGCTTTGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3416  
 QY 3746 CATGTTTGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3805  
 Db 3417 CATGTTTGCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3476  
 QY 3806 GGGATCTGAGTTCGACTTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3865

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Db 3477 AGGTCGCAATTTGATTTATTTAGATATCTTCTTGGCCGTCTGCGCATTTCCACGCT 3536
Qy 3866 CCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 3925
Db 3537 CTTGGGGGTTTCAATGAGATGTTCTGCTGCTGCTTTATCTTTCTTTGGACCGTG 3596
Qy 3926 TCCCTGAGTGTCTCAGACCAAGCGCTTGAACCGCTGCCCCACACCTTCCCTGAGCCACC 3965
Db 3597 TCCCTGAGTGTCTCAGACCAAGCGCTTGAACCGCTGCCCCACACCTTCCCTGAGCCACC 3656
Qy 3986 CCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 4045
Db 3657 TCCCTGAGTGTCTCAGACCAAGCGCTTGAACCGCTGCCCCACACCTTCCCTGAGCCACC 3716
Qy 4046 CGACTCGAGATATGTTCCAGACGACAGTGTCAAGGCTCAGAGGAGTCTTGGCCTA 4105
Db 3717 CGACTCGAGATATGTTCCAGACGACAGTGTCTGAGTGTGAGGAGTCTTGGCCTA 3776
Qy 4106 CGAGCGCCAGACGAGCGCGGAGGCGCTGCGCCACCAATGATCGTGAAGCGCAGAAAA 4165
Db 3777 CGAGCGCCAGACGAGCGCGGAGGCGCTGCGCCACCAATGATGTGAGGAGCGCAGAAAA 3836
Qy 4166 CCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 4225
Db 3837 CCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 3896
Qy 4226 CCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 4285
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Qy 4286 GCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 4345
Db 3957 GCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 4016
Qy 4346 GCGTTTGAATTTCTACTGAAGGCGATTTGCGCTTGAAGGCGCGCTGCGGCGCC 4405
Db 4017 GCGTTTGAATTTCTACTGAAGGCGATTTGCGCTTGAAGGCGCGCTGCGGCGCC 4076
Qy 4406 TCGCGGCGCGCTTCTCACAACCTCGGAGACCGGCTGCGGAGGAGGAGTCCGT 4465
Db 4077 CCGTGGGGCGCGTTCTCACAACCTCGGAGACCGGCTGCGGAGGAGGAGTCCGT 4136
Qy 4466 GCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 4525
Db 4137 GCGCGGCGTTTCATGATGGGCTGTTTGTCTCCGCTTTTGTCTTTCTTTGGACCATA 4196
Qy 4526 GCAACCGCGCGCTGCTGCGGCGCTGCGGAGGAGGAGTCTGCGGCGAG---- 4581
Db 4197 GCAATCCCGCG-----CCTGAGACCTGGGCGGAGGAGGAGGAGGAGTCTGCGGCGTA 4250
Qy 4582 -----GCTACCGCTGAGAGTGAACGAGGCGGCTTTTGAAGACCGCGGCTTCCAGCT 4636
Db 4251 TGAAGAGTACCGCTGAGAGTGAACGAGGCGGCTTTTGAAGAGTCTTCTTCTTTTCACT 4310
Qy 4637 CCGGCTGAGAGGAGGAGTGAAGGAGTGAAGTCAATGAGCTGAGAGAGTGAAGTGA 4696
Db 4311 CAGGTGAGAGGAGGAGTGAAGGAGTGAAGTCAATGAGCTGAGAGAGTGAAGTGA 4370
Qy 4697 GGAAGGCGCGCGGAGGAGGAGTGAAGGAGTGAAGTCAATGAGCTGAGAGAGTGA 4756
Db 4371 GGAAGGCGCGCGGAGGAGGAGTGAAGGAGTGAAGTCAATGAGCTGAGAGAGTGA 4430
Qy 4757 AAGATTTGGAAGGAGGAGGAGGAGTGAAGGAGTGAAGTCAATGAGCTGAGAGAGTGA 4816
Db 4431 AAGATTTGGAAGGAGGAGGAGGAGTGAAGGAGTGAAGTCAATGAGCTGAGAGAGTGA 4489
Qy 4817 AGTTATGGAAGGAGGAGGAGGAGTGAAGGAGTGAAGTCAATGAGCTGAGAGAGTGA 4876
Db 4490 AATATATG-----GGAAGGAGTCAATGAGTGAAGTGAAGTGAAGTGAAG 4530
Qy 4877 TTATTTTGTAAATATTTCTATAAATATTTAAGAGATGACACATGTGTAAATATAGAG 4936

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Db 4531 TTATTKGGAATAATTTCTATAAATTTAARAGGTGTACAA--TGTAAATACATG 4588
Qy 4937 GAGAGTGTAAAGTGTATGATCTGGGCTTCTCCACTCTCTGCCACAGAGTGTGAGGCC 4996
Db 4589 AATGCTGTACAGT--CTATTTCTGGGCGCTTCCACTCTGCCACAGAGTGTGAGGCC 4647
Qy 4997 ACAGTGGGCGCTTCCGATTTGTGATGAGGCTCCGCTGCCACAAACAGCTTCAATGAT 5056
Db 4648 ACA--GGGCGCTTCCGCTGTGTATGATTTGTGTCTGTGTGTGTGTGTGTGTGTGT 4705
Qy 5057 CTAAA-----TTTACGATATGTTCTGCTGCTTAAATATTTATATTTACTGT 5108
Db 4706 TTTTAAAAAATCTCCAGCATATGTCCGCTGCTTAAATATTTATATTTACTGT 4765
Qy 5109 AATATTTAATGAAATTTGATTTATGATTTATTTATTTATTTATTTATTTATTTATTT 5168
Db 4766 AATATTTAATGAAATTTGATTTATGATTTATTTATTTATTTATTTATTTATTTATTT 4824
Qy 5169 AATATTTAATTTGATTTATGATTTATTTATTTATTTATTTATTTATTTATTTATTT 5228
Db 4825 AATATTTAATTTGATTTATGATTTATTTATTTATTTATTTATTTATTTATTTATTT 4884
Qy 5229 AATGCTGTACAGT--CTATTTCTGGGCGCTTCCACTCTGCCACAGAGTGTGAGGCC 5280
Db 4885 AATGCTGTACAGT--CTATTTCTGGGCGCTTCCACTCTGCCACAGAGTGTGAGGCC 4931

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RESULT 8
US-08-954-668-9
; Sequence 9, Application US/08954668
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Elliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,668
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SUV-003.06
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-954-668-9

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Query Match 71.9%; Score 3801.2; DB 13; Length 5187;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

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OY	4817	AGTATGGAAGAAGTACCCGTGCCAGACAGAGTCATTGGTTACTGTAACGATTTGA			4876
Dd	4490	AATTAG-----		GGAAGCGACTTCATTGTTACTGTAACGATTTGA	4530
OY	4877	TATATTTGTTAAATATTTCTATAAATATTTAAGAGATGTACACATGHTAATATVAGAAC			4936
Dd	4531	TATTTTCTGGAATATTTCTATATAATTTAAAGAGTGTCACACA - TGTAATATACATVG			4588
OY	4937	GAAAGTGTAAAGTGGTATGATGCATGCGGGCTTCACCCTCGCCGCCAGAGTGTGAGAGCC			4996
Dd	4589	AAATGCTGTACACT-CTATTTTCTGGGGCCTCTCACATCTCGCCCAGAGTGGGGAACC			4647
OY	4997	ACAGTGGGCGCTCTCCGTAATTTGTGATGGGCTCCGTGCACAAACCAAGCTTATTAGT			5056
Dd	4648	ACA--GGGCGCCTTTCCCGTGTGATCATTTGTCGTCTGTGCACAAACCAAGCTTATTAG			4705
OY	5057	CCTAAA-----TTTCAGCATATGTGTGCTGCTCTTAAATATGTATTAATTTACTTGT			5108
Dd	4706	TTTTTAAAAAAATCTCCGACATATGTGCTGTGCTTTAAATATGTATTAATTTACTTGT			4765
OY	5109	ATAATTTCTATGCATAATATTGCTATGTAAATAGCAATTTTGTAAAGCTTCGTTAAA			5168
Dd	4766	ATAATTTCTATGCATAATATTGCTATGTAAATAGCAATTTTGTAAAGCTTCGTTAAA			4824
OY	5169	ATAATTTTAAATTTGCATATACACACCCTGTGTAGTATGAATGTACTGTAACTTTCA			5228
Dd	4825	ATAATTTTAAATTTGCATATACACACCCTGTGTAGATGATGTAATGTAACTTTCACTTTTG			4884
OY	5229	AACAGCGTATGCGTATATTTTGTGTTAATAGACAGATATGAAAGAAAGC			5280
Dd	4885	AACAGCGTATGCGTATATTTTGTGTTAATAGACAGATATGAAAGAAAGC			4931

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RESULT 9
US-08-954-701A-3
; Sequence 3, Application US/08954701A
; GENERAL INFORMATION:
; APPLICANT: SCOTT, MATHEW P
; APPLICANT: GOODRICH, LISA V
; APPLICANT: JOHNSON, RONALD L
; TITLE OF INVENTION: Patched Genes and their Use
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/954,701A
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36709
; REFERENCE/DOCKET NUMBER: SIU-003.08
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-7000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5187 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
;
US-08-954-701A-3

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[illegible]

QY 1466 GACCATGTTCCAGTTATGACTCCCAAGCAAAATGTACGAGCATTCAAGGGGTACAGATA 1525  
DB 1137 AACCATGTTCCAGTTATGACTCCCAAGCAAAATGTATGAGACTTACAGGGGTACAGATA 1196  
QY 1526 TGTCTGACACATCAACTGGAAGAGAGCAAAAGCGGAGCCATTCCTGAGGGCTGGCAGAG 1585  
DB 1197 TGTCTGACACATCAACTGGAAGAGAGCAAAAGCGGAGCCATTCCTGAGGGCTGGCAGAG 1256  
QY 1586 GACATATGTGAGAGTGTATCATGAGAGTGTGACAGAGACTCCACTCAAAAGGTCTTTC 1645  
DB 1257 GACTTACGTGAGAGTGTATCATGAGAGTGTGACAGAGACTCCACTCAAAAGGTCTTTC 1316  
QY 1646 CTTTACACACAGAGCCCTGGAGAGATTCCTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1705  
DB 1317 CTTTACACACAGAGCCCTGGAGAGATTCCTGAGAGTGTGAGAGTGTGAGAGTGTGAG 1376  
QY 1706 CGTGGCCAGCGGCTACTTACTCATGCTCGCCTATGCTTAAACCATGCTGGCCTGGGA 1765  
DB 1377 AGTGGCCAGCGGCTACTTACTCATGCTCGCCTATGCTTAAACCATGCTGGCCTGGGA 1436  
QY 1766 CTGCTCCAACTCCAGAGGTGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1825  
DB 1437 CTGCTCCAACTCCAGAGGTGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1496  
QY 1826 GGGTCGAGAGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1885  
DB 1497 GGGTCGAGAGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1556  
QY 1886 GGGTCGAGAGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1945  
DB 1557 GGGTCGAGAGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGG 1616  
QY 1946 GTTTCAGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2005  
DB 1617 GTTTCAGTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1676  
QY 2006 GAAGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2065  
DB 1677 GAAGCGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1736  
QY 2066 GGGCGCGTAAATCCGCTCTGCGGGCTGCGGGCTGCGGGCTGCGGGCTGCGGGCTGCG 2125  
DB 1737 GGGCGCGTAAATCCGCTCTGCGGGCTGCGGGCTGCGGGCTGCGGGCTGCGGGCTGCG 1796  
QY 2126 GGTATTAATTTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185  
DB 1797 GGTATTAATTTTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856  
QY 2186 TCGACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2245  
DB 1857 TCGACGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916  
QY 2246 AGTGAATTCAGGTTGAGCTGAGGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 2305  
DB 1917 AGTGAATTCAGGTTGAGCTGAGGCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1976  
QY 2306 CCGACGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2365  
DB 1977 CCGACGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2036  
QY 2366 TGTTCACGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2425  
DB 2037 CGTTCACGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2096  
QY 2426 GCGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2485  
DB 2097 ACCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2156  
QY 2486 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2545  
DB 2157 TCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2216

QY 2546 CTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2605  
DB 2217 CTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2276  
QY 2606 TCCCTTCTCTGAAACCAAAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2665  
DB 2277 TCCCTTCTCTGAAACCAAAAGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2336  
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DB 2337 GGGGGTCCAGCTTTATGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2396  
QY 2726 ACCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2785  
DB 2397 TCCCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2456  
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DB 2457 CAACATGTATATGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2516  
QY 2846 CTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2905  
DB 2517 CTTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2576  
QY 2906 CAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2965  
DB 2577 CAAATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2636  
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DB 2637 TGAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2696  
QY 3026 CTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3085  
DB 2697 CTTTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2756  
QY 3086 GTTGAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3145  
DB 2757 GTTGAATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2816  
QY 3146 CTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3205  
DB 2817 CTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2876  
QY 3206 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3265  
DB 2877 CCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2936  
QY 3266 GAGAAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3325  
DB 2937 GAGAAATCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2996  
QY 3326 GGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3385  
DB 2997 ACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3056  
QY 3386 TACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3445  
DB 3057 TACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3116  
QY 3446 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3505  
DB 3117 CATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3176  
QY 3506 CGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3565  
DB 3177 AGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3236  
QY 3566 GCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3625  
DB 3237 TGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3296  
QY 3626 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3685

Db 3297 GCGTGGGTCATCTCTATTTGATCTGTTGGCATGAGGTGAGTTCACGCTGACGCTGAGC 3356  
 Qy 3686 TTTGGCTTTTGACGGCCATCGCGACAGAAACCGGAGGCGTGTCTTGGCCCTGAGCA 3745  
 Db 3357 TTTGGCTTTTGACAGCCATTTGGGAGACAGAACACAGGGCTATGCTGCTGTGGAACA 3416  
 Qy 3746 CATGTTGACACCGCTCTGATGAGCGCCGTGTCACTCTGCTGGAGTGTGATGCTGCG 3805  
 Db 3417 CATGTTGCTCCCGTCTGACGCGTGTGCTCACCTGCTGCTGCTACTGATGCTTGC 3476  
 Qy 3806 GGGATGAGTTCAGTCTATGTCAGGATTTCTTGTGCTGCTGCGGGAGTTCACCACT 3865  
 Db 3477 AGGGTCCGAATTGATTTCTATTTGTCAGATACTTCTTGGCGTCTGGCCATTTCTACGT 3536  
 Qy 3866 CCTGGCGCTTCTCAATGAGCGGTGTTTGTCTCCGCTGCTTGTGCTTGTGGAACATA 3925  
 Db 3537 CTGGGGGTTCTCAATGAGCATGTTGTGCTGCTGCTCTTATCTCTTGTGGAACGTG 3596  
 Qy 3926 TCTGTAGGTGTCTCCAGCCCAAGCGCTTGAACCGCTGCCACACCTCCCTGAGCCACC 3985  
 Db 3597 TCTGTAGGTGTCTCCAGCCCAATGCGCTTGAACCGACTGCGCCACTCTGCGAGCCGCC 3656  
 Qy 3986 CCCGACGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4045  
 Db 3657 TCCAGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3716  
 Qy 4046 CGACTGAGTATAGTTCACAGACGACAGTGTGAGCGCTGACGAGAGAGTTCGCGACTA 4105  
 Db 3717 CGACTGAGTATAGTTCACAGACGACAGTGTGAGCGATGAGTGTGAGCGATGAGCAATA 3776  
 Qy 4106 CGAGCGCCAGAGGCGCGCGGAGGCGCTGCCACCAAGTATCGTGGAAAGCCAGAAAA 4165  
 Db 3777 CGAAGCAGAGAGGCGCGCGGAGGCGCTGCCACCAAGTATGAGTGTGAGCGACAGAAAA 3836  
 Qy 4166 CCCGCTTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4225  
 Db 3837 CCCGCTTGTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3896  
 Qy 4226 CCCGAGACAGAGCCCGCTGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4285  
 Db 3897 CCCGAGACAGAGCCCGCTGAGCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3956  
 Qy 4286 GCCCGGAGAGGAGCCCGCCAGAGAGGCTGTGGCCACCCCTCTACACACCGCGCAGAGA 4345  
 Db 3957 GCGTGAAGAGGAGCCCGCCAGAGAGGCTGTGGCCACCCCTCTACACACCGCGCAGAGA 4016  
 Qy 4346 GCGTGAAGAGGAGCCCGCCAGAGAGGCTGTGGCCACCCCTCTACACACCGCGCAGAGA 4405  
 Db 4017 GCGTGAAGAGGAGCCCGCCAGAGAGGCTGTGGCCACCCCTCTACACACCGCGCAGAGA 4076  
 Qy 4406 TCGCGGGGCGCGCTGTCACAAACCTCGGAACCCAGCTGCACTGCGCATGGGAGCTCCGT 4465  
 Db 4077 CCGTGGGGCGCGCTGTCACAAACCTCGGAACCCAGCTGCACTGCGCATGGGAGCTCCGT 4136  
 Qy 4466 GCCCGGCTACTGCGACCCCTACACACTGTGAGCGGCTTCTGCTGCTGCTGCTGCTGCT 4525  
 Db 4137 GCGCAGCTACTGCGACCCCTACACACTGTGAGCGGCTTCTGCTGCTGCTGCTGCTGCT 4196  
 Qy 4526 GACCCCGCGCGCTGCTGCGGGCTGCGGGAACCCCGAGGGGAGCTCTGCGCCAG---- 4581  
 Db 4197 GCATCCCGG-----CTGAGACTGTGGGCGCCAAACCCCGAGGGGAGCTCTGCGCCAGCTA 4250  
 Qy 4582 -----GTAACCTGAGACTGACACCGCGCTGTTGAGAGACCCCGCATGCTTTCACAGT 4636  
 Db 4251 TGAGAGCTACCTGAGACTGATACAGGGGATATTGAGAGATCTCATGCGCTTTTCAGAT 4310  
 Qy 4637 CCGGTGTGAGAGAGGATTCGAAGGTGAGTGTGAGTGTGAGAGAGCTGAGAGCTGAGATGCA 4696  
 Db 4311 CAGGTGTGAGAGAGGAGTCTAAGGTGAGTGTGAGTGTGAGAGAGCTGAGATGCA 4370  
 Qy 4697 GGAGAGGCGCGCGGAGAGAGCTCAACTGAGGCTGATTAAGTGTGAGAGAGAGGCG 4756  
 ||||||| ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 4371 GGAGAGCGCGTGGGAGACGCTCCAACTGAGGGTAAATTAATCTGAAGCAAGAGGCC 4430  
 Qy 4757 AAGATTGGAACCCCGCCACCCACCTCTTTCAGAACTGCTTGAAGAGACTGTTGG 4816  
 Db 4431 AAGATTGGAAC--GCCCGCCCGCCACCTCTTTCAGAACTGCTTGAAGAGACTGTTGG 4489  
 Qy 4817 AGTTATGGAAGAAAGTGGCCCTGTGCGAGACAGACAGTTCATTGTTACTGTAAACGATTGTA 4876  
 Db 4490 AATTATG-----GGAGGACAGTTCATTGTTACTGTAACTGATGTGA 4530  
 Qy 4877 TTTATTTGTAATATTTCTAATAATTTAAGAGATGACATGTAATATATAGAG 4936  
 Db 4531 TTAATKGTGAATAATTTCTAATAATTTAARAGGTGACACA--TGTAAATATACATGG 4588  
 Qy 4937 GAAGATGTAAGTGTGATGATCTGCGGCTTCTCCACTGCTGCCAGAGTGTGAGGCC 4996  
 Db 4589 AATGCTGTACAGT--CTAATTTCTGCGGCGCTCTCCACTGCTGCCAGAGTGTGAGGCC 4647  
 Qy 4997 ACAGTGGGCGCTCTCCGATTTGTCATTTGAGGCTCCGTCACACCAAGCTTCATTAGT 5056  
 Db 4648 ACA--GGGGCGCTTCCCTGCTGTACATTTGCTGTGCTGCCAACCAAGCTTACTAGT 4705  
 Qy 5057 CTTAAA-----TTGACATATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5108  
 Db 4706 TTTTAAAAAAATCTCCAGATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4765  
 Qy 5109 ATAAATCTATGCAAAATATGCTATGTAATAGATATTTGTAAGGTTTCTGTTAA 5168  
 Db 4766 ATAAATCTATGCAAAATATGCTATGTAATAGATTA--TTGTAAAGCTTTTCTGTTAA 4824  
 Qy 5169 ATAAATTTAAATTTGCAATATCAACACCTGTGTAGTATGAATGTTACTGTTAACTTCA 5228  
 Db 4825 ATAAATTTAAATTTGCAATATCAACACCTGTGTAGTATGAATGTTACTGTTAACTTTC 4884  
 Qy 5229 AACACGTCATGATGATTTTGTGTTATGAGCAGATATGAGAAAGC 5280  
 Db 4885 AACACGTCATGATGATTTTGTGTTATGAGCAGATATGAGAAAGC 4931  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 10  
 US-08-954-701A-9  
 : Sequence 9, Application US/08954701A  
 : GENERAL INFORMATION:  
 : APPLICANT: SCOTT, MATHEW P  
 : APPLICANT: GOODRICH, LISA V  
 : APPLICANT: JOHNSON, RONALD L  
 : TITLE OF INVENTION: Patched Genes and their use  
 : NUMBER OF SEQUENCES: 19  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Foley, Hoag & Elliot  
 : STREET: One Post Office Square  
 : CITY: Boston  
 : STATE: MA  
 : COUNTRY: USA  
 : ZIP: 02109  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: ASCII(text)  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/954,701A  
 : FILING DATE: 20-Oct-1997  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Vincent, Matthew P.  
 : REGISTRATION NUMBER: 36709  
 : REFERENCE/DOCKET NUMBER: SUV-003,08  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 617-832-1000  
 : TELEFAX: 617-832-7000  
 : INFORMATION FOR SEQ ID NO: 9:  
 : SEQUENCE CHARACTERISTICS:  
 :

: LENGTH: 5187 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : US-08-954-701a-9

Query Match 71.9%; Score 3801.2; DB 13; Length 5187;  
 Best Local Similarity 88.1%; Pred. No. 0;  
 Matches 4276; Conservative 3; Mismatches 516; Indels 57; Gaps 11;

QY 446 CGTCCGCCGCGGAGCGGCGCTGAGGCGGAGCGCGACAGCGGAGCGGCGCGCG 505  
 DB 120 CGGGGCCCTGGGAGCGAGCGCGCGCGGAGCGCGACAGCGGAGCGGAGCGCG 179  
 QY 506 TGTGCGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 555  
 DB 180 C--GCGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 236  
 QY 566 TCTGAGAGAGATTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 625  
 DB 237 TCTGAGAGAGATTTTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 296  
 QY 626 GAAGTTTCAGAGAGCTTTATTTAACTGGCTTTTACATTTCAAAAAAACTGCGCAAGTT 685  
 DB 297 GAAGTTTCAGAGAGCTTTATTTAACTGGCTTTTACATTTCAAAAAAACTGCGCAAGTT 356  
 QY 686 CTGAGTTGGGCGCTCCATATTTGGGCGCTTCCGCGGAGGAGGAGGAGGAGGAGGAG 745  
 DB 357 TTTGGTTGGGCTCTCTCTCATATTTGGGCGCTTCCGCGGAGGAGGAGGAGGAGGAG 416  
 QY 746 CGAGACCAAGCTGAGAGAGCTGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 805  
 DB 417 CGAGACCAAGCTGAGAGAGCTGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 476  
 QY 806 TTATATCTGCCAGAGATTTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 865  
 DB 477 TTATATCTGCCAGAGATTTGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 536  
 QY 866 CCTTAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 925  
 DB 537 TCCAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 596  
 QY 926 GGCATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 985  
 DB 597 AGCACTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 656  
 QY 986 TTTGCTTACAAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1045  
 DB 657 TTTGCTTACAAATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 716  
 QY 1046 ATATCTTACACCTTTGATATATACACCTTTGAGGAGGAGGAGGAGGAGGAGGAG 1105  
 DB 717 ATATCTTACACCTTTGATATATACACCTTTGAGGAGGAGGAGGAGGAGGAGGAGGAG 776  
 QY 1106 ACACTCTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1165  
 DB 777 ACAGTCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 836  
 QY 1166 TTTGGAATTTCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1225  
 DB 837 CTTGGAATTTCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 896  
 QY 1226 GCTGAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1285  
 DB 897 GCTGAATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 956  
 QY 1286 TCCAGACTCCCGCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1345  
 DB 957 CCCAGATTTGCCCTGCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1016  
 QY 1346 TGTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1405

DB 1017 TGTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076  
 QY 1406 GATTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1465  
 DB 1077 GATTGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1136  
 QY 1466 GACCATGTTCCAGTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1525  
 DB 1137 AACCATGTTCCAGTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1196  
 QY 1526 TGTCTCACACATTCATCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1585  
 DB 1197 TGTCTCACACATTCATCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1256  
 QY 1586 GACATATGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1645  
 DB 1257 GACTTACGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1316  
 QY 1646 CTTCACACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1705  
 DB 1317 CTTCACACACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1376  
 QY 1706 CGTGGCCAGCGGCTTACTTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1765  
 DB 1377 AGTGGCCAGCGGCTTACTTATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1436  
 QY 1766 CTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1825  
 DB 1437 CTGCTCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1496  
 QY 1826 GGCCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1885  
 DB 1497 GGCCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1556  
 QY 1886 GGTTTTGCATTTTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1945  
 DB 1557 GGTTTTGCATTTTCTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1616  
 QY 1946 CTTTCAAGTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2005  
 DB 1617 ATTTCAGTAAACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1676  
 QY 2006 GAACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2065  
 DB 1677 CAACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1736  
 QY 2066 GGCCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2125  
 DB 1737 GGCCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1796  
 QY 2126 GGTGTTCAATTTTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2185  
 DB 1797 GGTGTTCAATTTTCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1856  
 QY 2186 TCGACGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2245  
 DB 1857 CAGACGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1916  
 QY 2246 AGTATTTACAGGTTAACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2305  
 DB 1917 GGTGATTTCAAGTTTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1976  
 QY 2306 CCCACCTCCCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2365  
 DB 1977 CCCACCTCCCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2036  
 QY 2366 TGTTCACCTCCCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2425  
 DB 2037 GGTTCACCTCCCTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2096  
 QY 2426 GCGCTCCGAGATCTCTGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2485



Db 2097 ACCGCTGAGATCTCTGTACAGCCTGTTACCGTTCACCCAGACAACTTCAGCTGTGAGAG 2156  
 Qy 2486 CCCAGAGAGACACGACTCCACAGAGGACCTGCTCCAGTTCCTCGAGCTCCAGCTCCA 2545  
 Db 2157 TCCGAGAGAGACACGACTTACAGAGGACCTGCTCCAGTTCCTCGAGCTCCAGCTCCA 2216  
 Qy 2546 CTGCTCTGAGACCCCTCTGTACAGAGTGACACTCTCATCTTTTGTGAGAGCAGTATGC 2605  
 Db 2217 CTGCTCTGAGACCCCTCTGTACAGAGTGACACTCTCTGTTTGTGAGAGAGCAGTATGC 2276  
 Qy 2606 TCTTTTCTCTGTAAACCAAAAGCAAGTATGATGATCTCTCTTTTCTGGGGCTGCT 2665  
 Db 2277 TCTTTTCTCTGTAAACCAAAAGCAAGTATGATGATCTCTCTTTTCTGGGGCTGCT 2336  
 Qy 2666 GGGGGTCAAGCTTTATGTGACACACCCAGTAGAGACGGGCTGACCTTACGGACATTTGT 2725  
 Db 2337 GGGGGTCAAGCTTTATGTGAGACACCCAGTAGAGACGGGCTGACCTTACGGACATTTGT 2396  
 Qy 2726 ACCTCGGGAAACCAAGAAATATGACTTTATTTGCTGCACAAATTCAAATTCCTTTCTTTC 2785  
 Db 2397 TCCCCGGGAAACCAAGAAATATGACTTTATTTGCTGCACAAATTCCTTTCTTTC 2456  
 Qy 2786 CAACATGATATAGTACCCCGAAGAGAGACTACCCGAATATCCGACACTTACTTTAGCA 2845  
 Db 2457 CAACATGATATAGTACCCCGAAGAGAGACTACCCGAATATCCGACACTTACTTTAGCA 2516  
 Qy 2846 CCTACACAGAGAGTTTCAAGTACAGTAAATGATGATGTTTGAAGAAACAAACAGCTTCC 2905  
 Db 2517 CCTTCAATAGAGTTTCAAGTACAGTAAATGATGATGTTTGAAGAAACAAACAGCTTCC 2576  
 Qy 2906 CAAATATGCTGCTGACACTTACAGAGCTGCTTCAAGGAGCTTTCAGAGATGATGATTTGACAG 2965  
 Db 2577 CCAAAATGCTGCTGACACTTACAGAGCTGCTTCAAGGAGCTTTCAGAGATGATGATTTGACAG 2636  
 Qy 2966 TGAATGGGAAACCGGAAATCATGCCCAAAATTAACAAGATGATGATGATGATGATGATGAT 3025  
 Db 2637 TGAATGGGAAACCGGAGGATCATGCCCAAAATTAACAAGATGATGATGATGATGATGATGAT 2696  
 Qy 3026 CCTTGCCTTACAAACTCTGTGTGCAACCGGAGCGGAGATGATGATGATGATGATGATGATGAT 3085  
 Db 2697 CCTTGCCTTACAAACTCTGTGTGCAACCGGAGCGGAGATGATGATGATGATGATGATGATGAT 2756  
 Qy 3086 GTTGAATTAACACAGCTTGTGTGCAACCGGAGCGGAGATGATGATGATGATGATGATGATGAT 3145  
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 Qy 3146 CTACCTGAGCGCTTGGGTGCAACGAGACCCGCTGCGATGCTGCTGCCAGGCCAACAT 3205  
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 Qy 3206 CCGGCCACACCGACAGAAATGGGTCCAGACAAAGCCGACTACATGCTGGAACAAAGGCT 3265  
 Db 2877 CCGGCCCTACCGGCCGAGAGGTCATGACAAAGCCGACTACATGCTGGAACAAAGGCT 2936  
 Qy 3266 GAGAAATCCCGGAGAGAGAGCCCATGAGTATGCCAGTTCCTTTTCTACCTCAACGGGTT 3325  
 Db 2937 GAGAAATCCCGAGAGAGAGCCCATGAGTATGCCAGTTCCTTTTCTACCTCAACGGGCT 2996  
 Qy 3326 GGGGAGACACTTACAGCTTTTGGAGCAATTGAAAAGTAAAGACATCTGAGCAACTA 3385  
 Db 2997 AGGAGACACTTACAGCTTTTGGAGCAATTGAAAAGTAAAGACATCTGAGCAACTA 3056  
 Qy 3386 TACGAGACCTGGGGCTGTCCAGTTACCCCAAGGCTACCCCTTCTCTTCTGTGGAGCAGTA 3445  
 Db 3057 TACGAGACCTGGGGCTGTCCAGTTACCCCAAGGCTACCCCTTCTCTTCTGTGGAGCAGTA 3116  
 Qy 3446 CATGGGCTTCCCGCAGCTGGGTGCTGCTGCTTATAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3505  
 Db 3117 CATGACCTTCCCGCAGCTGGGTGCTGCTGCTTATAGGCTGCTGCTGCTGCTGCTGCTGCTGCT 3176  
 Qy 3506 CCGTGGCTGCTTCTCTTCTGAAACCCCTGAGAGCGGCGGAGATGATGATGATGATGATGATGAT 3565  
 Db 3177 AGTGGCGAGTCTTCTCTCTGAAACCCCTGAGAGCGGCGGAGATGATGATGATGATGATGATGAT 3236

Qy 3566 GCTGATGAGCGGTGAGCTGTGTGGCAATGATGGGCTTCATCGAATCAAGCTCACTGCCGT 3625  
 Db 3237 TCTGATGAGCGGTGAGCTGTGTGGCAATGATGGGCTTCATCGAATCAAGCTCACTGCCGT 3296  
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 Qy 3686 TTTGGCTTTTCTGAGAGGCGCATGGGCAACAAGACCCGAGGGCTGTGCTTGCCTGAGCA 3745  
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 Qy 3746 CATGTTTGCACCCGCTCTGATGGGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3805  
 Db 3417 CATGTTTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3476  
 Qy 3806 GGGATCTGAGTTCGACTTCATTTGTAGGTAATTTCTTTTGTGTGCTGCTGCTGCTGCTGCTGCT 3865  
 Db 3477 AGGGTCCGAATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 3536  
 Qy 3866 CCTGCGGCTTCTCATTTGGCTGCTGCTTCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3925  
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 Db 3597 TCTGAGGTGCTTCCAGCAACCGGCTTGAACCGGCTTGAACCGGCTTGAACCGGCTTGAACCGGCT 3656  
 Qy 3986 CCCCAGCGTGTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTT 4045  
 Db 3657 TCCAAAGTGTGCTGCTGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCTTCCGCT 3716  
 Qy 4046 CGACTCGGAGTATTTCTTCCAGACAGACAGTGTAGGCTTCCAGGAGAGCTTGGGCACTA 4105  
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 Qy 4106 CGAGGCCGAGAGGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4165  
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 Db 4137 GCGCGGCTTACGAGCGGCTTACGAGCGGCTTACGAGCGGCTTACGAGCGGCTTACGAGCGGCTTACGAG 4196  
 Qy 4526 GCAACCGCGGCTTCTGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGGCTTCTGCGG 4581  
 Db 4197 GCAACCGCGGCTTCTGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGGCTTCTGCGGCGGCTTCTGCGG 4250  
 Qy 4582 GCTTACCTGAGAGTACGAGGCTTCTGAGGAGGCTTCTGAGGAGGCTTCTGAGGAGGCTTCTGAGGAG 4636  
 Db 4251 TGAGAGCTACCTGAGAGTACGAGGCTTCTGAGGAGGCTTCTGAGGAGGCTTCTGAGGAGGCTTCTGAGG 4310









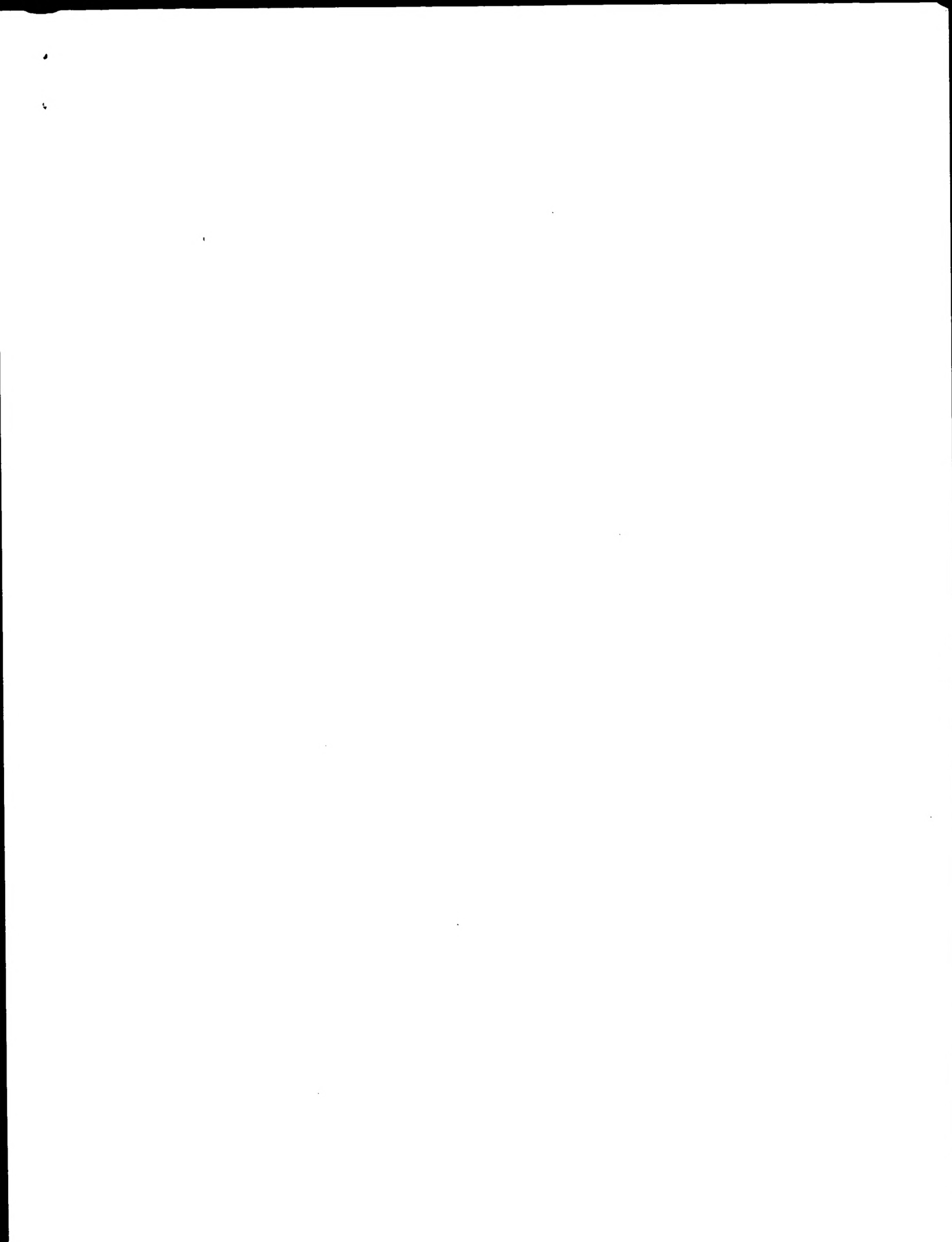








Db	626	ggccgcgcggatgccacagttgacccaacctggatccagagcaagcgcctcgaggagagcttggct	685
Oy	1191	AAATTAACATATCAAGTGGACAGCTGGGAGAGAAATGCTGAATTAAGCTGAGGTGGTCAAT	1250
Db	686	cccttgccttccctcttgaaggcttccggagag---ctgtatgaacaaggacaaagtglygcag	742
Oy	1251	GGTTCATGTGAGACGCCCTCCCTGCTCAATTCGGGCCATCCAGACTGCTCCCGCACAGCCCC	1310
Db	743	gctcagtgaggcgcccttctgcacccctgaattgacctccacgcgcgcacccatgctcccc	802
Oy	1311	AACAAAAATTCACCAAACTCTTGATATGACCCTTTGTAATGGTGAATGTCATGAC	1370
Db	803	aaccatcacagcagcagcagctcccaatggtctcacagctgaagtggggctgcctag	862
Oy	1371	TTATCCGAAGAAGTATATGACTGGACAGAGAGTGTGTTGGTGGCCACAGTCACAGC	1430
Db	863	ttctccacaatattcatgacctgagcaggaggaattgcttgcctggaaagcatgycacaagac	922
Oy	1431	AGCACTGGAAACTCGTCAGCGGCCATGCCCCGACACATGTTGTCAGTTAATGACTCCC	1490
Db	923	ccccaaaggagagctgtcgtgagggcagggccctcgagcaacctctgcctgagtagctcc	982
Oy	1491	AAGCAATGTGACGACGACTTCAAGGGGTACGAGTATGTTCTCACACATCAACTGGAACGAG	1550
Db	983	cgccacatctgacaggaacttccggagggtgacatccacatacagacatgacattgctgagtgag	1042
Oy	1551	GACCAAGCGGACCCATCTCGTAGAGGCTGGCCACAGACATATGCGAGGTGGTTTCAACAG	1610
Db	1043	gagcagagccagacagtgctacaaagcttcggcagcgcgcttctgcaagcgcggccagag	1102
Oy	1611	AGGTGTGGCACGAACTCCACTCAAAAGGTGCTTTCTTCACACACAGACCCCTGGAGAC	1670
Db	1103	ggccctgcgtgagaaagcttcccagagatccatgaccttccctcccaaccacctgagtaac	1162
Oy	1671	ATTCCTAAATCCCTTCTGTCAGACGACATGTCATCCGGGTGGCCAGCGGTACTACATCAG	1730
Db	1163	atctctgcatgagcttctctgaagtcagtgctgcgcgcggtggtgaggtacatctgcatag	1222
Oy	1731	CTCGCCTATGCCGTGTAAACCATGATGCGCTGGAGCTGCTCCAAAGTCCAGGGTGCCTG	1790
Db	1223	cttgcctctatgacctggtgacacatgctcggttggactgcgcccaggtcccaaggtctcg	1282
Oy	1791	GGGCTGTGGCGGCTCGCTGGTGTGACATGTACATGGCTGCGAGGACTGGGCGCTGTGCTCA	1850
Db	1283	ggccttgcgcggggtactgcctcgtggccttgcgggtgaggtccctgaagccttgcgtcttgcc	1342
Oy	1851	TTGATCGAATTTCTCTTAACGCTGCMAACATCCAGCTTTGGCATTTCCGCTTTGGT	1910
Db	1343	ctgcctgagatcacctcaatgctgcacatacccaagtgctgcaccttcttgctcctcgggaa	1402
Oy	1911	GTGGGTGTCGATGATGTTTCTTTCTTGCGCCCAAGCCTTCATGTAACAGACAGAAATAAA	1970
Db	1403	atcgcgcgtgagatgacgtattctctgttgcgtgcacatgctccacagagctctgc-----ct	1456
Oy	1971	AGAAATCCCTTTGAGGACAGCAGCGGGGAGTGCTCGTAACGCGACAGAGACCGAGCGGCGC	2030
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Oy	2031	CTCACGTCATCAGCAATGTCAACAGCTTTCTTATGCGCGGCTTAATCCCAATTCGCCGT	2090
Db	1517	ctcacatccatcaacaacaatgycgccttccctcatgctgcctctcgltcccatccctcg	1576
Oy	2091	CTGCGGGCGTTTCTCCCTCCAGGCACGGGTAG 2121	
Db	1577	ctgcgagaccttctcttcaagccatccctcag 1607	



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: January 13, 2001, 06:12:42 ; Search time 2793.3 Seconds

(without alignments)  
13265.884 Million cell updates/sec

Title: US-08-656-055-18

Perfect score: 5288

Sequence: 1 GATTCGGGAGCGCAAG.....TATGAGAGAGCCCGAATT 5288

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
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13: gb\_est13:\*  
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190: gb\_gss25:\*  
191: gb\_gss26:\*  
192: gb\_gss27:\*  
193: gb\_gss28:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	566	10.7	566	28	AL044174	AL044174 DKFZP434P0428.1
2	498.4	9.4	653	106	BE263745	BE263745 601192194
3	484.6	9.2	496	28	AL046751	AL046751 DKFZP434P0428.1
4	462.4	8.7	475	105	BE244165	BE244165 TCBPAP1E12
5	422.4	8.0	437	28	AL120137	AL120137 DKFZP761G
6	410.4	7.8	657	104	BE109565	BE109565 UI-R-BJ1-
7	379	7.2	476	104	BE106695	BE106695 UI-R-BJ1-
8	317.6	6.0	402	19	AI326577	AI326577 mm33b11.Y
9	316	6.0	329	21	AI494319	AI494319 qy98607.X
10	306	5.8	422	3	AA171645	AA171645 z094c07.X
11	300.6	5.7	475	15	AI045038	AI045038 UI-R-C1-K
12	300.2	5.7	305	105	BE243347	BE243347 TCBPAP1D12
13	299.4	5.7	312	135	BE765294	BE765294 IL2-NF010
14	299.4	5.7	314	17	AI239549	AI239549 qh31f06.X
15	290.4	5.5	511	91	AW528449	AW528449 UI-R-BJ1-
16	289.8	5.5	585	159	AO608259	AO608259 HS_5409_B
17	288.8	5.5	336	3	AA169807	AA169807 z094c07.X
18	287.2	5.4	403	2	AA080038	AA080038 mm33b11.Y
19	275	5.2	464	1	AA030749	AA030749 m31h01.T
20	269.8	5.1	473	107	BE335795	BE335795 us06f10.X
21	263.4	5.0	310	5	AA328411	AA328411 EST31889
22	259.4	4.9	273	26	AI880090	AI880090 ap31b06.X
23	253.8	4.8	580	173	AZ498012	AZ498012 IM0335005
24	249.2	4.7	397	89	AW314277	AW314277 10252 MAR
25	243.6	4.6	436	106	BE292080	BE292080 601085808
26	243	4.6	550	135	BE757000	BE757000 211327 MA
27	240	4.5	253	21	AI494442	AI494442 qy99403.X
28	239	4.5	451	8	AA517095	AA517095 vH8C10.T
29	214.8	4.1	495	137	BE938361	BE938361 RCO-TN007
30	193.2	3.7	316	102	BI188695	BI188695 BI188695
31	186.4	3.5	331	5	AA329006	AA329006 EST32560
32	177.6	3.4	184	15	AI018356	AI018356 ov41b02.S
33	176	3.3	1101	190	CNS017V5	AL108539 Drosophila
34	156.4	3.0	364	23	AI705049	AI705049 UI-R-GO-U
35	156	3.0	946	192	CNS03EU0	AL240875 Tetraodon
36	153.6	2.9	285	102	BI190274	BI190274 BI190274
37	140	2.6	287	136	BE843857	BE843857 RCO-TN007
38	137	2.6	201	25	AI842476	AI842476 UI-R-AM1-
39	136.2	2.6	1022	192	CNS03EU0	AL240873 Tetraodon
40	124.4	2.4	175	26	AI885389	AI885389 w193d12.X
41	122.8	2.3	513	165	AZ012766	AZ012766 RPCI-23-3
42	118.2	2.2	689	106	BE282024	BE282024 601100075
43	116.6	2.2	375	139	C63129	C63129 C63129 Yui1
44	116	2.2	573	105	BE234509	BE234509 141639 MA
45	102.2	1.9	279	149	AO097628	AO097628 HS_3039_B

## ALIGNMENTS

RESULT 1  
LOCUS AL044174 566 bp mRNA  
DEFINITION DKFZP434P0428.1 434 (synonym: htes3) Homo sapiens CDNA clone  
ACCESSION AL044174  
VERSION AL044174.1 GI:5432399  
KEYWORDS EST.  
SOURCE human.





QY 1533 CACATCACTGGAACGAGACAAACCGGACCCATCTGTGAGGCGCTGAGAGACATAT 1592  
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 Db 301 CACATCACTGGAACGAGACAAACCGGACCCATCTGTGAGGCGCTGAGAGACATAT 360  
 QY 1593 GTGAGAGTGTTCATCAGAGTGTGCGACAGACTCCATCCAAAGGTGCTTCTCCAC 1652  
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 Db 361 GTGAGAGTGTTCATCAGAGTGTGCGACAGACTCCATCCAAAGGTGCTTCTCCAC 420  
 QY 1653 ACCAGACCCCTGAGACATCTGAAATCTCTGTAGTCAAGTGTATCCGCTGAGCC 1712  
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 Db 421 ACCAGACCCCTGAGACATCTGAAATCTCTGTAGTCAAGTGTATCCGCTGAGCC 480  
 QY 1713 AGCGGCTACTTACTGATGCT 1732  
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 Db 481 AGCGGCTACTTACTGATGCT 500  
 RESULT 3  
 AL046751 496 bp mRNA EST 29-FEB-2000  
 LOCUS DKE2P4341179\_r1.434 (synonym: htes3) Homo sapiens cDNA clone  
 DEFINITION DKE2P4341179 5', mRNA sequence.  
 ACCESSION AL046751  
 VERSION AL046751.1 GI:5434813  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 496)  
 AUTHORS Poustka, A., Klein, M., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
 TITLE EST (Poustka, et al.)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Poustka A.J.  
 Department Leinrach  
 Max-Planck-Institute for Molecular Genetics  
 Ihnestrasse 73, 14195 Berlin, Germany  
 Tel: +49-30-84131623  
 Fax: +49-30-84131128  
 Email: poustka@imping-berlin-dahlem.mpg.de  
 This is the 5' sequence of the clone insert  
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
 Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;  
 sequenced by DKFZ (German Cancer Research Center,  
 Heidelberg/Germany) within the CDNA sequencing consortium of the  
 German Genome Project.  
 No sl sequence available.  
 This clone (DKE2P4341179) is available at the RZPD in Berlin.  
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
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 /organism="Homo sapiens"  
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 /lab\_host="DH10B"  
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 ORIGIN  
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 Best Local Similarity 99.2%; Pred. NO. 9.5e-105;  
 Matches 487; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 4798 CTTAAGAGAACTGTTGAGTTATGAAAGATGCGCTGTCCAGACAGCATTCATT 4857  
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 Db 1 CTTAAGAGAACTGTTGAGTTATGAAAGATGCGCTGTCCAGACAGCATTCATT 60  
 QY 4858 GTTACTGTAACCGATTGTATTATTGTTAAATATTCTATAAATTAAAGAGATGTAC 4917  
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Db 61 GTTACTGTAACCGATTGTATTATTGTTAAATATTCTATATAAATTAAAGAGATGTAC 120  
 QY 4918 ACATGTGTATATAGGAAGAGAGATGTAAAGTGTATGATGTGGGCTTCTCCACTCT 4977  
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 Db 121 ACATGTGTATATAGGAAGAGAGATGTAAAGTGTATGATGTGGGCTTCTCCACTCT 180  
 QY 4978 GCGCCAGAGTGTGAGGCGACAGTGGGCGCTCCGCTATTGTGTAGTGGGCTCCGTCGC 5037  
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 Db 301 AATTACTGTATATTTTATGCAAAATTTGTTATGTAATGTAATTTTGTAAAGT 360  
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 Db 361 TTCTGTTAAATATTTTAAATTTTGCATATCAACACCCGTGTAGTATGAATGTTACT 420  
 QY 5218 GTTAACCTTTCACCAACCGCTATGCGTGAATATTTTGTGTTAATGACAGATATGAAGA 5277  
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 Db 421 GTTAACCTTTCACCAACCGCTATGCGTGAATATTTTGTGTTAATGACAGATATGAAGA 480  
 QY 5278 AGCCCGAAT 5288  
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 Db 481 AGCCCGAAT 491  
 RESULT 4  
 BE244165 475 bp mRNA EST 13-JUL-2000  
 LOCUS TCBAP1258 pediatric pre-B cell acute lymphoblastic leukemia  
 DEFINITION Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP1258, mRNA  
 sequence.  
 ACCESSION BE244165  
 VERSION BE244165.1 GI:9095905  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 475)  
 AUTHORS Wei, Y., Tsang, Y.T.M., Mel, G., Ku, J.M., Ali-Osman Jr., F.R., Muzny, D.  
 TITLE Pediatric Leukemia cDNA Sequencing Project  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Dr. Judith F. Margolin  
 Human Genome Sequencing Center at Baylor College of Medicine and  
 Texas Children's Cancer Center  
 One Baylor Plaza, Houston, TX 77030, USA  
 Tel: 713 770 4536  
 Fax: 713 770 4038  
 Email: jmargin@leccc.org  
 Seq primer: M13 primer.  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="TCBAP1258"  
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 /lab\_host="DH10B"  
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REFERENCE 1 (bases 1 to 657)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 JOURNAL discovery  
 MEDLINE Genome Res. 6 (9), 791-806 (1996)  
 COMMENT 97044477  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: mscares@blue.weeg.uiowa.edu  
 Oligo-dt track not found. Not 1 site shown in beginning of sequence  
 is likely internal to the message. cDNA library Preparation: M.B.  
 Soares Lab Clone distribution: Clones will be available through  
 Research Genetics (www.resgen.com) The following repetitive  
 elements were found in this cDNA sequence: 144-315,  
 >C-rich#low complexity  
 Seq primer: M13 Forward  
 POLYA-No.

FEATURES  
 source Location/Qualifiers

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 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-B01-asr-b-04-0-UI"  
 /clone\_1lb="UI-R-B01"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; The UI-R-B01  
 library is a subtracted library derived from the following  
 tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV  
 canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,  
 AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.  
 For a detailed description of the library from which this  
 clone was derived, please visit our web site at  
 ratseq.uiowa.edu. The subtraction has been previously  
 described in (Bonaldo, Lennon and Soares, Genome Research  
 6:791-806, 1996)  
 "R6-Seq-None found"  
 BASE COUNT 130 a 194 c 227 g 106 t  
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Query Match 7.8% Score 410.4; DB 104; Length 657;  
 Best Local Similarity 79.4%; Pred. No. 2.2e-90;  
 Matches 610; Conservative 0; Mismatches 46; Indels 112; Gaps 6;

QY 101 CGGCCGAGAGACCT-CGGGACCCCGCGCATGTGGCAATGGAAGCGCGAGGTCTGAC 159  
 Db 1 CGGCCGAGAGACCTCGCGGACCTCAGCGGCATGTGGCAATGGAAGCGCGAGGTCTGAG 60  
 QY 160 TCCCGCGAGCGCGCGCGCGCGAGCGGACAGGCGCCCGTGTGAGCAGCAGCAGCG 219  
 Db 61 TCCCGCGAGCGCGCGCGCGCGAGCGGACAGGCGCCCGTGTGAGCAGCAGCAGCG 120  
 QY 220 GCTGCTGTCATCAGCGAGCGCGCGCGAGCGGACAGGCGCGGCTCTCTCGCAG 279  
 Db 121 ----GCTGTGTACCGGAGCGCGAGTCC-----CGGCGCGCAGCAGAGGTCTCTCGCAG 171  
 QY 280 CCGAGCGCGCGCGCGCGCGCGAGCGGACAGGCGGCGCGCGCGCGCGCGCG 339  
 Db 172 CCGAGCGCGCGCGCGCGCGCGCGCGAGCGC----- 198  
 QY 340 GAAGCTTCCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 399  
 Db 199 -----GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231  
 QY 400 ACGCCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 459  
 Db 232 ACGCCGCG-----CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 252

QY 460 GCGCGCTGAGAGCGGAGCGCGAGCGGAGCGGCGGCGCGCGCGCGCGCGCGCG 519  
 Db 233 GCGAGCGCGCGCGCGCGCGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 309  
 QY 520 ACCGGAGCTATCTGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 579  
 Db 310 ACCGGAGCTATCTGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 369  
 QY 580 CCAAGGGGAGGCTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 639  
 Db 370 CCAAGGGGAGGCTACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 429  
 QY 640 TCTATTATTAAGCTGCTTACATTCATAAATAATCGCGCAAGTCTTGTTGCGCC 699  
 Db 430 TCTATTATTAAGCTGCTTACATTCATAAATAATCGCGCAAGTCTTGTTGCGCG 489  
 QY 700 TCCCTATTTTGGGCGCTTCCGCGTGGGATTAACAGCAGCACTTCGAGACCACTGG 759  
 Db 490 TCCCTATTTTGGGCGCTTCCGCGTGGGATTAACAGCAGCACTTCGAGACCACTGG 549  
 QY 760 AGGAGCTGGGGTGCAGGTTGGAGCAGAGTAAGTGTGAATTAAATTACTGCGCAGA 819  
 Db 550 AGGAGCTGGGGTGCAGGTTGGAGCAGAGTAAGTGTGAATTAAATTACTGCGCAGA 609  
 QY 820 AGATTGGAGAGAGGCTATTTTATCTCACTCACTGATATGACAGCC 867  
 Db 610 AGATTGGAGAGAGGCTATTTTATCTCACTCACTGATATGACAGCTC 657

RESULT 7  
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 LOCUS UI-R-B01-asr-b-04-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone  
 DEFINITION UI-R-B01-asr-b-04-0-UI 3', mRNA sequence.  
 BE106695  
 ACCESSION BE106695.1 GI:8498797  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Norway rat.  
 Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 Rattus.

REFERENCE 1 (bases 1 to 476)  
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
 TITLE Normalization and subtraction: two approaches to facilitate gene  
 JOURNAL discovery  
 MEDLINE Genome Res. 6 (9), 791-806 (1996)  
 COMMENT 97044477  
 Contact: Soares, MB  
 Program for Rat Gene Discovery and Mapping  
 University of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 Tel: 319 335 8250  
 Fax: 319 335 9565  
 Email: mscares@blue.weeg.uiowa.edu  
 Oligo-dt track not found. Not 1 site shown in beginning of sequence  
 is likely internal to the message. cDNA library Preparation: M.B.  
 Soares Lab Clone distribution: Clones will be available through  
 Research Genetics (www.resgen.com)  
 Seq primer: M13 Forward  
 POLYA-No.

FEATURES  
 source Location/Qualifiers

1..476  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-B01-asr-b-04-0-UI"  
 /clone\_1lb="UI-R-B01"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pT73D-Pac (Pharmacia) with a modified  
 polylinker. Site 1: Not I; Site 2: Eco RI; The library  
 (UI-R-B01) is a subtracted library derived from a mixture









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/sex="male"
/tissue_type="leukopheresis"
/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
/clone="vector: lambda psb: Site_1: BamHI; Site_2: EcoRI;
First strand cDNA was primed with an anchored
XhoI-oligo(dT) primer [5'-GGAGGACTCGAGCGCCGAGGAGGAG(1)VN
3'; V-A,C,G; N-A,C,G,T] and then dg tailed. Second
strand was primed with a BamHI-dc primer
[5'-AGAGGCTCGGATCGCGCCGCAATTAATATAT(C) 3'].
Double-stranded cDNA was then digested with BamHI and SalI
XhoI and directionally cloned into the BamHI and SalI
sites of lambda psb vector. Library went through one
round of normalization. Library was constructed by Wei
Yu"

```

```

BASE COUNT      107 a      62 c      48 g      88 t
ORIGIN
Query Match      5.7%; Score 300.2; DB 105; Length 305;
Best Local Similarity 99.0%; Pred. No. 2.9e-63;
Matches 302; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 4886 TTAATATTTCTAATAATATTAAAGATGTACACATGTATATATAGAGAGAGAGATGT 4945
|||||
DB 305 TAAATATTCTATTAATATTAAAGATGTACACATGTATATATAGAGAGAGAGATGT 246
|||||
QY 4946 AAGTGGTATGATCTGGGGCTTCGACATCTGCCAGAGTGTGAGCCACAGTGGG 5005
|||||
DB 245 AAGTGGTATGATCTGGGGCTTCGACATCTGCCAGAGTGTGAGCCACAGTGGG 186
|||||
QY 5006 CCTTCGCTATTTGGCATTTGGGCTCGGTCGACACCAAGCTTCATAGCTTAAATTT 5065
|||||
DB 185 CCTTCGCTATTTGGCATTTGGGCTCGGTCGACACCAAGCTTCATAGCTTAAATTT 126
|||||
QY 5066 CAGCATATGTGCTGCTGCTTAAATATTGATATTTACTTTGATTAATTTGATCAATA 5125
|||||
DB 125 CAGCATATGTGCTGCTGCTTAAATATTGATATTTACTTTGATTAATTTGATCAATA 66
|||||
QY 5126 TTGCTTATGTAATAGATTTATTTGTAAGGTTTCTGTTTAAATATTGATTTGAT 5185
|||||
DB 65 TTGCTTATGTAATAGATTTATTTGTAAGGTTTCTGTTTAAATATTGATTTGAT 6
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QY 5186 ATCAC 5190
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DB 5 ATCAC 1

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RESULT 13
BE765294      312 bp      mRNA      EST      19-SEP-2000
LOCUS      BE765294
DEFINITION      IL2-NT0102-160600-105-603 NT0102 Homo sapiens cDNA, mRNA sequence.
ACCESSION      BE765294
VERSION      BE765294.1 GI:10195218
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

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REFERENCE
AUTHORS      Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE      Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE      20202663
COMMENT      Contact: Simpson A.J.G.
Laboratory of Cancer Genetics

```

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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4tl2-IL2-NT0102-160
600-105-603&tl3=2000-06-16&tl4=1)
Seq primer: puc 18 forward
High quality sequence stop: 311.
Location/Qualifiers
1. 312
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0102"
/dev_stage="Adult"
/clone="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

```

BASE COUNT      41 a      83 c      88 g      100 t
ORIGIN
Query Match      5.7%; Score 299.4; DB 135; Length 312;
Best Local Similarity 99.7%; Pred. No. 4.6e-63;
Matches 300; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

QY 3627 CCGGTGTCATCCTGATGCTCTGTTGGCATAGAGTGAATTCACCGTTACGTTGCT 3686
|||||
DB 3 CCGGTGTCATCCTGATGCTCTGTTGGCATAGAGTGAATTCACCGTTACGTTGCT 62
|||||
QY 3687 TTGGCTTTTGACGGCCATCGGCCACAGAACCCGAGGCTGTGCTGCGCCGAGCAC 3746
|||||
DB 63 TTGGCTTTTGACGGCCATCGGCCACAGAACCCGAGGCTGTGCTGCGCCGAGCAC 122
|||||
QY 3747 ATGTTTGACCCGCTGATGAGCGCGCTGTCACATCTGCTGAGTGTGATGCTGGCG 3806
|||||
DB 123 ATGTTTGACCCGCTGATGAGCGCGCTGTCACATCTGCTGAGTGTGATGCTGGCG 182
|||||
QY 3807 GGATCTGATGCTGATTTGTCAGATTTTCTTGTGCTGCTGCGCATCTCACATC 3866
|||||
DB 183 GGATCTGATGCTGATTTGTCAGATTTTCTTGTGCTGCTGCGCATCTCACATC 242
|||||
QY 3867 CTCGGCTTCTCAATGGCGGTTTGGTCCGCTTTGCTTTGCTTTGACCATAT 3926
|||||
DB 243 CTCGGCTTCTCAATGGCGGTTTGGTCCGCTTTGCTTTGCTTTGACCATAT 302
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QY 3927 C 3927
DB 303 C 303

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```

RESULT 14
AI239549      314 bp      mRNA      EST      01-DEC-1998
LOCUS      AI239549
DEFINITION      GH31f06.x1 Soares NFL.T GBC.S1 Homo sapiens cDNA clone
IMAGE:1846307 3' similar to TR-013635 013635 PATCHED. ; contains
TARI.T3 TARI repetitive element ; , mRNA sequence.
ACCESSION      AI239549
VERSION      AI239549.1 GI:3834946
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

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REFERENCE
AUTHORS      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

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Db 198 -----GCAGCGCGCGCGCAACATGGCCCTGGCTGTAA 231
OY 401 CGCCGCCGAGCCCGAGACCGCGCGCGCGAGCGCTGTATCGTGCCCGGAGC 460
    |||||
Db 232 CGCCGC-----CGGGCCCTGGGCAG 252
OY 461 GCCGCTGAGCGCGGAGCGCAGACGAGCGGGGCTGCGCGCTGCTGGCGCGGA 520
    || ||| || ||||| ||||| || ||| |||||
Db 253 GCAGCGCGCGCGGAGCGCAGACCGGGGACCGCACCG--CGCGCGCGGA 309
OY 521 CGGAGCTATCTGCACCGCGCCAGCTACTGCGAGCGCGCTTCTGCTGTGAGCAGATTTC 580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 310 CGGAGCTATCTGCACCGCGCCAGCTACTGCGAGCGCGCTTCTGCTGTGAGCAGATTTC 369
OY 581 CAAGGGGAGGCTACTGCGCGGAAAGCGCCACTGTGCTGAGAGCGAAGTTTCAGAGACT 640
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 370 CAAGGGGAGGCTACTGCGCGGAAAGCGCGCTGTGCTGAGAGCGAAGTTTCAGAGACT 429
OY 641 CTTATTTAACTGGGTTTACATTCAAAAAACTGCGGCAAGTTCTTGGTTGGGCT 700
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 430 CTTATTTAACTGGGTTTACATTCAAAAAACTGCGGCAAGTTTGGGTGGGCT 489
OY 701 CCTCATATTTGGGCTTCGC 721
    ||||| ||||| |||||
Db 490 CCTCATATTTGGGCTTCGC 510
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